INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

| (51) International Patent Classification 7 : | | (11) International Publication Number: WO 00/69884 |
|---|---|---|
| C07K | A2 | (43) International Publication Date: 23 November 2000 (23.11.00) |

(21) International Application Number: PCT/NZ00/00075

(22) International Filing Date: 15 May 2000 (15.05.00)

(30) Priority Data:
09/312,283     14 May 1999 (14.05.99)     US

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(81) Designated States: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published
*Without international search report and to be republished upon receipt of that report.*

(54) Title: COMPOSITIONS ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE

(57) Abstract

Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

# COMPOSITIONS ISOLATED FROM SKIN CELLS
# AND METHODS FOR THEIR USE

5   Technical Field of the Invention

This invention relates to polynucleotides encoding polypeptides, polypeptides expressed in skin cells, and various methods for treating a patient involving administration of a polypeptide or polynucleotide of the present invention.

10  Background of the Invention

The skin is the largest organ in the body and serves as a protective cover. The loss of skin, as occurs in a badly burned person, may lead to death owing to the absence of a barrier against infection by external microbial organisms, as well as loss of body temperature and body fluids.

15  Skin tissue is composed of several layers. The outermost layer is the epidermis which is supported by a basement membrane and overlies the dermis. Beneath the dermis is loose connective tissue and fascia which cover muscles or bony tissue. The skin is a self-renewing tissue in that cells are constantly being formed and shed. The deepest cells of the epidermis are the basal cells, which are enriched in 20  cells capable of replication. Such replicating cells are called progenitor or stem cells. Replicating cells in turn give rise to daughter cells called 'transit amplifying cells'. These cells undergo differentiation and maturation into keratinocytes (mature skin cells) as they move from the basal layer to the more superficial layers of the epidermis. In the process, keratinocytes become cornified and are ultimately shed 25  from the skin surface. Other cells in the epidermis include melanocytes which synthesize melanin, the pigment responsible for protection against sunlight. The Langerhans cell also resides in the epidermis and functions as a cell which processes foreign proteins for presentation to the immune system.

The dermis contains nerves, blood and lymphatic vessels, fibrous and fatty 30  tissue. Within the dermis are fibroblasts, macrophages and mast cells. Both the epidermis and dermis are penetrated by sweat, or sebaceous, glands and hair follicles.

Each strand of hair is derived from a hair follicle. When hair is plucked out, the hair re-grows from epithelial cells directed by the dermal papillae of the hair follicle.

When the skin surface is breached, for example in a wound, the stem cells proliferate and daughter keratinocytes migrate across the wound to reseal the tissues. The skin cells therefore possess genes activated in response to trauma. The products of these genes include several growth factors, such as epidermal growth factor, which mediate the proliferation of skin cells. The genes that are activated in the skin, and the protein products of such genes, may be developed as agents for the treatment of skin wounds. Additional growth factors derived from skin cells may also influence growth of other cell types. As skin cancers are a disorder of the growth of skin cells, proteins derived from skin that regulate cellular growth may be developed as agents for the treatment of skin cancers. Skin derived proteins that regulate the production of melanin may be useful as agents which protect skin against unwanted effects of sunlight.

Keratinocytes are known to secrete cytokines and express various cell surface proteins. Cytokines and cell surface molecules are proteins which play an important role in the inflammatory response against infection and also in autoimmune diseases affecting the skin. Genes and their protein products that are expressed by skin cells may thus be developed into agents for the treatment of inflammatory disorders affecting the skin.

Hair is an important part of a person's individuality. Disorders of the skin may lead to hair loss. Alopecia areata is a disease characterized by the patchy loss of hair over the scalp. Total baldness is a side effect of drug treatment for cancer. The growth and development of hair are mediated by the effects of genes expressed in skin and dermal papillae. Such genes and their protein products may be usefully developed into agents for the treatment of disorders of the hair follicle.

New treatments are required to hasten the healing of skin wounds, to prevent the loss of hair, enhance the re-growth of hair or removal of hair, and to treat autoimmune and inflammatory skin diseases more effectively and without adverse effects. More effective treatments of skin cancers are also required. There thus remains a need in the art for the identification and isolation of genes encoding

proteins expressed in the skin, for use in the development of therapeutic agents for the treatment of disorders including those associated with skin.

## Summary of the Invention

5      The present invention provides polypeptides expressed in skin cells, together with polynucleotides encoding such polypeptides, expression vectors and host cells comprising such polynucleotides, and methods for their use.

In specific embodiments, isolated polynucleotides are provided that comprise a DNA sequence selected from the group consisting of: (a) sequences recited in SEQ

10     ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (b) complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-119, 198-

15     276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (e) sequences having a 99% probability of being the same as a sequence of (a)-(d); and (f) sequences having at least 50%, 75% or 90% identity to a sequence of (a)-(d).

In further embodiments, the present invention provides isolated polypeptides comprising an amino acid sequence selected from the group consisting of: (a)

20     sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, together with isolated polynucleotides encoding such polypeptides. Isolated polypeptides which comprise at least a functional portion of a

25     polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; and (b) sequences having 50%, 75% or 90% identity to a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, are also provided.

30     In related embodiments, the present·invention provides expression vectors comprising the above polynucleotides, together with host cells transformed with such vectors.

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In a further aspect, the present invention provides a method of stimulating keratinocyte growth and motility, inhibiting the growth of epithelial-derived cancer cells, inhibiting angiogenesis and vascularization of tumors, or modulating the growth of blood vessels in a subject, comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398.

Methods for modulating skin inflammation in a subject are also provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 338 and 347; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 338 and 347. In an additional aspect, the present invention provides methods for stimulating the growth of epithelial cells in a subject. Such methods comprise administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 129 and 348; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 129 and 348.

In yet a further aspect, methods for inhibiting the binding of HIV-1 to leukocytes, for the treatment of an inflammatory disease or for the treatment of cancer in a subject are provided, the methods comprising administering to the subject a composition comprising an isolated polypeptide including an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 340, 344, 345 and 346; and (b) sequences having at least 50%, 75% or 90% identity to a sequence provided in SEQ ID NOS: 340, 344, 345 and 346.

As detailed below, the isolated polynucleotides and polypeptides of the present invention may be usefully employed in the preparation of therapeutic agents for the treatment of skin disorders.

The above-mentioned and additional features of the present invention, together with the manner of obtaining them, will be best understood by reference to the

following more detailed description. All references disclosed herein are incorporated herein by reference in their entirety as if each was incorporated individually.

Brief Description of the Drawings

5      Fig. 1 shows the results of a Northern analysis of the distribution of huTR1 mRNA in human tissues. Key: He, Heart; Br, Brain; Pl, Placenta; Lu, Lung; Li, Liver; SM, Skeletal muscle; Ki, Kidney; Sp, Spleen; Th, Thymus; Pr, Prostate; Ov, Ovary.

Fig. 2 shows the results of a MAP kinase assay of muTR1a and huTR1a. MuTR1a (500ng/ml), huTR1a (100ng/ml) or LPS (3pg/ml) were added as described
10    in the text.

Fig. 3 shows the stimulation of growth of neonatal foreskin keratinocytes by muTR1a.

Fig. 4 shows the stimulation of growth of the transformed human keratinocyte cell line HaCaT by muTR1a and huTR1a.

15     Fig. 5 shows the inhibition of growth of the human epidermal carcinoma cell line A431 by muTR1a and huTR1a.

Fig. 6 shows the inhibition of IL-2 induced growth of concanavalin A-stimulated murine splenocytes by KS2a.

Fig. 7 shows the stimulation of growth of rat intestinal epithelial cells (IEC-
20    18) by a combination of KS3a plus apo-transferrin.

Fig. 8 illustrates the oxidative burst effect of TR-1 (100 ng/ml), muKS1 (100 ng/ml), SDF1$\alpha$ (100 ng/ml), and fMLP (10 $\mu$M) on human PBMC.

Figure 9 shows the chemotactic effect of muKS1 and SDF-1$\alpha$ on THP-1 cells.

Figure 10 shows the induction of cellular infiltrate in C3H/HeJ mice after
25    intraperitoneal injections with muKS1 (50 $\mu$g), GV14B (50 $\mu$g) and PBS.

Figure 11 demonstrates the induction of phosphorylation of ERK1 and ERK2 in CV1/EBNA and HeLa cell lines by huTR1a.

Figure 12 shows the huTR1 mRNA expression in HeLa cells after stimulation by muTR1, huTR1, huTGF$\alpha$ and PBS (100 ng/ml each).

30     Figure 13 shows activation of the SRE by muTR1a in PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells.

Figure 14 shows the inhibition of huTR1a mediated growth on HaCaT cells by an antibody to the EGF receptor.

Figure 15A shows the nucleotide sequence of KS1 cDNA (SEQ ID NO: 464) along with the deduced amino acid sequence (SEQ ID NO: 465) using single letter code. The 5' UTR is indicated by negative numbers. The underlined NH2-terminal amino acids represent the predicted leader sequence and the stop codon is denoted by ***. The poly-adenylation signal is marked by a double underline. Figure 15B shows a comparison of the complete open reading frame of KS1 (referred to in Fig. 15B as KLF-1) with its human homologue BRAK and with the mouse α-chemokines mCrg-2, mMig, mSDF-1, mBLC, mMIP2, mKC and mLIX. An additional five residues are present in KS1 and BRAK between cysteine 3 and cysteine 4 that have not previously been described for chemokines.

Detailed Description of the Invention

In one aspect, the present invention provides polynucleotides that were isolated from mammalian skin cells. As used herein, the term "polynucleotide" means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and RNA molecules, both sense and anti-sense strands. The term comprehends cDNA, genomic DNA, recombinant DNA and wholly or partially synthesized nucleic acid molecules. A polynucleotide may consist of an entire gene, or a portion thereof. A gene is a DNA sequence that codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion et al., "Anti-sense Techniques," *Methods in Enzymol.* 254(23):363-375, 1995; and Kawasaki et al., *Artific. Organs* 20(8):836-848, 1996.

Identification of genomic DNA and heterologous species DNAs can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a cDNA sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be

used to amplify and identify genomic and cDNA sequences. Synthetic DNAs corresponding to the identified sequences and variants may be produced by conventional synthesis methods. All the polynucleotides provided by the present invention are isolated and purified, as those terms are commonly used in the art.

5        In specific embodiments, the polynucleotides of the present invention comprise a DNA sequence selected from the group consisting of sequences provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464, and variants of the sequences of SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464. Polynucleotides that comprise complements of such
10      DNA sequences, reverse complements of such DNA sequences, or reverse sequences of such DNA sequences, together with variants of such sequences, are also provided.

         The definition of the terms "complement," "reverse complement," and "reverse sequence," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse
15      sequence are as follows:

|                     |                |
|---------------------|----------------|
| complement          | 3' TCCTGG 5'   |
| reverse complement  | 3' GGTCCT 5'   |
| reverse sequence    | 5' CCAGGA 3'.  |

         In another aspect, the present invention provides isolated polypeptides
20      encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide which comprises a partial isolated DNA sequence
25      provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as well as variants of such sequences.

         Polypeptides of the present invention may be produced recombinantly by
30      inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may

be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, insect, yeast, or a mammalian
5    cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the
10   group consisting of sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be
15   made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the
20   polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below.

Portions and other variants of the inventive polypeptides may also be
25   generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method,
30   where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin

Elmer/Applied BioSystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, T., *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985).

5      Sections of DNA sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

10     In certain preferred embodiments, described in detail below, the isolated polypeptides are incorporated into pharmaceutical compositions or vaccines for use in the treatment of skin disorders.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more

15     nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 50%, more preferably at least 75%, and most preferably at least 90% identity to a sequence of the present invention. The percentage identity is determined by aligning the two

20     sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides in a specified region may be determined against another

25     polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The alignment and similarity of polypeptide sequences may be examined using the BLASTP and algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences

30     translated in all reading frames against polypeptide sequences. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (ftp://ncbi.nlm.nih.gov) under /blast/executables/. The FASTA and FASTX

algorithms are available on the Internet at the ftp site ftp://ftp.virginia.edu/pub/. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of polynucleotide variants. The readme files for FASTA and FASTX v1.0x that are distributed with the

5      algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is also described in Pearson, WR and Lipman, DJ, "Improved Tools for Biological Sequence Analysis," *PNAS* 85:2444-2448, 1988; and Pearson WR, "Rapid and Sensitive Sequence Comparison with FASTP and FASTA," *Methods in Enzymology* 183:63-98, 1990.

10     The BLASTN algorithm version 2.0.4 [Feb-24-1998], set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm version 2.0.4, set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use

15     in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX is described at NCBI's website at URL http://www.ncbi.nlm.nih.gov/BLAST/newblast.html and in the publication of Altschul, Stephen F., *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of

20     protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with default parameters thus: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i

25     queryseq –o results; and parameters are: -p  Program Name [String]; -d  Database [String]; -e  Expectation value (E) [Real]; -G  Cost to open a gap (zero invokes default behavior) [Integer]; -E  Cost to extend a gap (zero invokes default behavior) [Integer]; -r  Reward for a nucleotide match (blastn only) [Integer]; -v  Number of one-line descriptions (V) [Integer]; -b  Number of alignments to show (B) [Integer]; -i  Query

30     File [File In]; -o  BLAST report Output File [File Out]  Optional.  The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity for

polypeptides: blastall –p blastp –d swissprotdb –e 10 –G 1 –E 11 –r 1  –v 30 –b 30 –i
queryseq –o results; and the parameters are:  -p Program Name [String]; -d Database
[String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default
behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer];

5    -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show
(b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out]
Optional.

The "hits" to one or more database sequences by a queried sequence produced
by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar

10   portions of sequences.  The hits are arranged in order of the degree of similarity and
the length of sequence overlap.  Hits to a database sequence generally represent an
overlap over only a fraction of the sequence length of the queried sequence.

The percentage similarity of a polynucleotide or polypeptide sequence is
determined by aligning polynucleotide and polypeptide sequences using appropriate

15   algorithms, such as BLASTN or BLASTP, respectively, set to default parameters;
identifying the number of identical nucleic or amino acids over the aligned portions;
dividing the number of identical nucleic or amino acids by the total number of nucleic
or amino acids of the polynucleotide or polypeptide of the present invention; and then
multiplying by 100 to determine the percentage similarity.  By way of example, a

20   queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide
sequence in the EMBL database having 520 nucleic acids over a stretch of 23
nucleotides in the alignment produced by the BLASTN algorithm using the default
parameters.  The 23 nucleotide hit includes 21 identical nucleotides, one gap and one
different nucleotide.  The percentage identity of the queried polynucleotide to the hit

25   in the EMBL database is thus 21/220 times 100, or 9.5%.  The similarity of
polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for
polynucleotide and polypeptide alignments.  The Expect value (E) indicates the
number of hits one can "expect" to see over a certain number of contiguous sequences

30   by chance when searching a database of a certain size.  The Expect value is used as a
significance threshold for determining whether the hit to a database indicates true
similarity.  For example, an E value of 0.1 assigned to a polynucleotide hit is

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interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being the same. For sequences having an

5      E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides,

10     with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleic or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide

15     is any sequence that has at least a 99% probability of being the same as the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the

20     present invention that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99%

25     probability of being the same as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

Variant polynucleotide sequences will generally hybridize to the recited polynucleotide sequences under stringent conditions. As used herein, "stringent

30     conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in

1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

As used herein, the term "$x$-mer," with reference to a specific value of "$x$," refers to a polynucleotide or polypeptide, respectively, comprising at least a specified number ("$x$") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464; or any of the polypeptides set out in SEQ ID NO: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465. The value of $x$ may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues ($x$-mers) of any of the polynucleotides identified as SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464, or their variants. Polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues ($x$-mers) of any of the polypeptides identified as SEQ ID NO: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465. According to preferred embodiments, the value of $x$ is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NOS: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464, or of a variant of one of the polynucleotides provided in SEQ ID NO: 1-119, 198-274, 349-372, 399-405, 410-412, 416, 418-455 and 464. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, or of a variant of one of the polypeptides provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465.

The inventive polynucleotides may be isolated by high throughput sequencing of cDNA libraries prepared from mammalian skin cells as described below in

Example 1. Alternatively, oligonucleotide probes based on the sequences provided in SEQ ID NOS: 1-119, 198-274, 349-372,.399-405, 410-412, 416, 418-455 and 464 can be synthesized and used to identify positive clones in either cDNA or genomic DNA libraries from mammalian skin cells by means of hybridization or polymerase chain
5 reaction (PCR) techniques. Probes can be shorter than the sequences provided herein but should be at least about 10, preferably at least about 15 and most preferably at least about 20 nucleotides in length. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (see, for example, Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR*
10 *Technology*, Stockton Press: NY, 1989; (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

In addition, DNA sequences of the present invention may be generated by
15 synthetic means using techniques well known in the art. Equipment for automated synthesis of oligonucleotides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems Division (Foster City, California) and may be operated according to the manufacturer's instructions.

Since the polynucleotide sequences of the present invention have been derived
20 from skin, they likely encode proteins that have important roles in growth and development of skin, and in responses of skin to tissue injury and inflammation as well as disease states. Some of the polynucleotides contain sequences that code for signal sequences, or transmembrane domains, which identify the protein products as secreted molecules or receptors. Such protein products are likely to be growth
25 factors, cytokines, or their cognate receptors. Several of the polypeptide sequences have more than 25% similarity to known biologically important proteins and thus are likely to represent proteins having similar biological functions.

In particular, the inventive polypeptides have important roles in processes such as: induction of hair growth; differentiation of skin stem cells into specialized
30 cell types; cell migration; cell proliferation and cell-cell interaction. The polypeptides are important in the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of the disclosed polypeptides act as

modulators of immune responses, especially since immune cells are known to infiltrate skin during tissue insult causing growth and differentiation of skin cells. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of disease states not only within skin, but also in

5      other tissues of the body. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

In one aspect, the present invention provides methods for using one or more of

10     the inventive polypeptides or polynucleotides to treat disorders in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human.

In this aspect, the polypeptide or polynucleotide is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the

15     above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and a non-specific immune response amplifier, such as an adjuvant or a liposome, into which the polypeptide is incorporated.

Alternatively, a vaccine or pharmaceutical composition of the present

20     invention may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines and pharmaceutical compositions, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, and bacterial and viral expression systems. Appropriate nucleic acid expression

25     systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminator signal). Bacterial delivery systems involve the administration of a bacterium (such as Bacillus-Calmette-Guerin) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*,

30     vaccinia or other poxvirus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic, or defective, replication competent virus. Techniques for incorporating DNA into such expression systems are well known in the art. The DNA

may also be "naked," as described, for example, in Ulmer, *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

5       Routes and frequency of administration, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intradermal, intramuscular, intravenous, or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from

10      about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg per kg of host, and preferably from about 100 pg to about 1 µg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 ml to about 5 ml.

        While any suitable carrier known to those of ordinary skill in the art may be

15      employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax, or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine,

20      talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

25      Any of a variety of adjuvants may be employed in the vaccines derived from this invention to non-specifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a non-specific stimulator of immune responses, such as lipid A, *Bordetella pertussis*, or *M. tuberculosis*. Suitable

30      adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories, Detroit, Michigan), and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, New Jersey). Other suitable

adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A, and Quil A.

The polynucleotides of the present invention may also be used as markers for tissue, as chromosome markers or tags, in the identification of genetic disorders, and

5  for the design of oligonucleotides for examination of expression patterns using techniques well known in the art, such as the microarray technology available from Synteni (Palo Alto, California). Partial polynucleotide sequences disclosed herein may be employed to obtain full length genes by, for example, screening of DNA expression libraries using hybridization probes or PCR primers based on the inventive

10  sequences.

The polypeptides provided by the present invention may additionally be used in assays to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, in assays to quantitatively determine levels of protein or cognate corresponding ligand or receptor, as anti-inflammatory agents, and in compositions

15  for skin, connective tissue and/or nerve tissue growth or regeneration.


Example 1

ISOLATION OF CDNA SEQUENCES FROM SKIN CELL EXPRESSION LIBRARIES


20  The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed from specialized rodent or human skin cells as shown in Table 1.

Table 1

| Library | Skin cell type | Source |
|---------|----------------|--------|
| DEPA | dermal papilla | rat |
| SKTC | keratinocytes | human |
| HNFF | neonatal foreskin fibroblast | human |
| MEMS | embryonic skin | mouse |
| KSCL | keratinocyte stem cell | mouse |
| TRAM | transit amplifying cells | mouse |

These cDNA libraries were prepared as described below.

_cDNA Library from Dermal Papilla (DEPA)_

Dermal papilla cells from rat hair vibrissae (whiskers) were grown in culture and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

_cDNA Library from Keratinocytes (SKTC)_

Keratinocytes obtained from human neonatal foreskins (Mitra, R and Nikoloff, B in _Handbook of Keratinocyte Methods_, pp. 17-24, 1994) were grown in serum-free KSFM (BRL Life Technologies) and harvested along with differentiated cells ($10^8$ cells). Keratinocytes were allowed to differentiate by addition of fetal calf serum at a final concentration of 10% to the culture medium and cells were harvested after 48 hours. Total RNA was isolated from the two cell populations using TRIzol Reagent (BRL Life Technologies) and used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene). cDNAs expressed in differentiated keratinocytes were enriched by using a PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, California). Briefly, mRNA was obtained from either undifferentiated keratinocytes ("driver mRNA") or differentiated keratinocytes ("tester mRNA") and used to synthesize cDNA. The two populations of cDNA were separately digested with _Rsa_I to obtain shorter, blunt-ended molecules. Two tester populations were created by ligating different adaptors at the cDNA ends and two successive rounds of hybridization were performed with an excess of driver cDNA. The adaptors allowed for PCR amplification of only the differentially expressed sequences which were then ligated into T-tailed pBluescript (Hadjeb, N and Berkowitz, GA, _BioTechniques_ 20:20-22 1996), allowing for a blue/white selection of cells containing vector with inserts. White cells were isolated and used to obtain plasmid DNA for sequencing.

_cDNA library from human neonatal fibroblasts (HNFF)_

Human neonatal fibroblast cells were grown in culture from explants of human neonatal foreskin and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life

Technologies, Gaithersburg, Maryland), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, California), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

*cDNA library from mouse embryonic skin (MEMS)*

Embryonic skin was micro-dissected from day 13 post coitum Balb/c mice. Embryonic skin was washed in phosphate buffered saline and mRNA directly isolated from the tissue using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

*cDNA library from mouse stem cells (KSCL) and transit amplifying (TRAM) cells*

Pelts obtained from 1-2 day post-partum neonatal Balb/c mice were washed and incubated in trypsin (BRL Life Technologies) to separate the epidermis from the dermis. Epidermal tissue was disrupted to disperse cells, which were then resuspended in growth medium and centrifuged over Percoll density gradients prepared according to the manufacturer's protocol (Pharmacia, Sweden). Pelleted cells were labeled using Rhodamine 123 (Bertoncello I, Hodgson GS and Bradley TR, *Exp Hematol.* 13:999-1006, 1985), and analyzed by flow cytometry (Epics Elite Coulter Cytometry, Hialeah, Florida). Single cell suspensions of rhodamine-labeled murine keratinocytes were then labeled with a cross reactive anti-rat CD29 biotin monoclonal antibody (Pharmingen, San Diego, California; clone Ha2/5). Cells were washed and incubated with anti-mouse CD45 phycoerythrin conjugated monoclonal antibody (Pharmingen; clone 30F11.1, 10ug/ml) followed by labeling with streptavidin spectral red (Southern Biotechnology, Birmingham, Alabama). Sort gates were defined using listmode data to identify four populations: CD29 bright rhodamine dull CD45 negative cells; CD29 bright rhodamine bright CD45 negative cells; CD29 dull rhodamine bright CD45 negative cells; and CD29 dull rhodamine dull CD45 negative cells. Cells were sorted, pelleted and snap frozen prior to storage at -80°C. This protocol was followed multiple times to obtain sufficient cell numbers of each population to prepare cDNA libraries. Skin stem cells and transit amplifying cells are known to express CD29, the integrin β1 chain. CD45, a leucocyte specific

antigen, was used as a marker for cells to be excluded in the isolation of skin stem cells and transit amplifying cells. Keratinocyte stem cells expel the rhodamine dye more efficiently than transit amplifying cells. The CD29 bright, rhodamine dull, CD45 negative population (putative keratinocyte stem cells; referred to as KSCL),

5   and the CD29 bright, rhodamine bright, CD45 negative population (keratinocyte transit amplifying cells; referred to as TRAM) were sorted and mRNA was directly isolated from each cell population using the Quick Prep Micro mRNA purification kit (Pharmacia, Sweden). The mRNA was then used to prepare cDNA libraries as described above for the DEPA library.

10       cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer.


## Example 2

15   ### CHARACTERIZATION OF ISOLATED CDNA SEQUENCES

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithms FASTA and/or BLASTN. The corresponding predicted protein sequences (DNA translated to protein in each of 6 reading frames) were compared to sequences in the SwissProt database using the

20   computer algorithms FASTX and/or BLASTP. Comparisons of DNA sequences provided in SEQ ID NO: 1-119 to sequences in the EMBL DNA database (using FASTA) and amino acid sequences provided in SEQ ID NO: 120-197 to sequences in the SwissProt database (using FASTX) were made as of March 21, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 198-274 to sequences in

25   the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 275-348 to sequences in the SwissProt database (using BLASTP) were made as of October 7, 1998. Comparisons of DNA sequences provided in SEQ ID NO: 349-372 to sequences in the EMBL DNA database (using BLASTN) and amino acid sequences provided in SEQ ID NO: 373-398 to sequences in the SwissProt

30   database (using BLASTP) were made as of January 23, 1999. Comparisons of polynucleotide sequences provided in SEQ ID NO: 418-455 to sequences in the EMBL DNA database (using BLASTN) and polypeptide sequences provided in SEQ

ID NO: 456-463 to sequences in the SwissProt database (using BLASTP) were made as of April 23, 2000.

Isolated cDNA sequences and their corresponding predicted protein sequences were computer analyzed for the presence of signal sequences identifying secreted

5    molecules. Isolated cDNA sequences that have a signal sequence at a putative start site within the sequence are provided in SEQ ID NO: 1-44, 198-238, 349-358, 399, 418-434 and 440-449. The cDNA sequences of SEQ ID NO: 1-6, 198-199, 349-352, 354, 356-358 and 440 were determined to have less than 75% identity (determined as described above), to sequences in the EMBL database using the computer algorithms

10    FASTA or BLASTN, as described above. The predicted amino acid sequences of SEQ ID NO: 120-125, 275-276, 373-380 and 382 were determined to have less than 75% identity (determined as described above) to sequences in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above.

Further sequencing of some of the isolated partial cDNA sequences resulted in

15    the isolation of the full-length cDNA sequences provided in SEQ ID NOS: 7-14, 200-231, 372, 418-422, 441-448. The amino acid sequences encoded by the cDNA sequences of SEQ ID NO: 7-14, 200-231 and 372 are provided in SEQ ID NOS: 126-133, 277-308 and 396, respectively. The cDNA sequences of SEQ ID NO: 418-422 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO 7 and

20    11-14, namely SEQ ID NO: 126, and 130-133, respectively.

Comparison of the full length cDNA sequences with those in the EMBL database using the computer algorithm FASTA or BLASTN, as described above, revealed less than 75% identity (determined as described above) to known sequences. Comparison of the amino acid sequences provided in SEQ ID

25    NOS: 126-133 and 277-308 with those in the SwissProt database using the computer algorithms FASTX or BLASTP, as described above, revealed less than 75% identity (determined as described above) to known sequences.

Comparison of the predicted amino acid sequences corresponding to the cDNA sequences of SEQ ID NOS: 15-23 with those in the EMBL database using the

30    computer algorithm FASTA database showed less than 75% identity (determined as described above) to known sequences. These predicted amino acid sequences are provided in SEQ ID NOS: 134-142.

Further sequencing of some of the isolated partial cDNA sequences resulted in the isolation of full-length cDNA sequences provided in SEQ ID NOS: 24-44, 232-238, 423-434 and 449. The amino acid sequences encoded by the cDNA sequences of

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SEQ ID NO: 24-44, 232-238 and 429 are provided in SEQ ID NOS: 143-163, 309-315 and 456, respectively. The cDNA sequences of SEQ ID NO: 423-428, 430-434 and 449 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 27-29, 34, 35, 37, 40-44 and 238, namely SEQ ID NO: 146-148, 153, 154,

5    156, 159-163 and 315, respectively. These amino acid sequences were determined to have less than 75% identity, determined as described above to known sequences in the SwissProt database using the computer algorithm FASTX.

Isolated cDNA sequences having less than 75% identity to known expressed sequence tags (ESTs) or to other DNA sequences in the public database, or whose

10   corresponding predicted protein sequence showed less than 75% identity to known protein sequences, were computer analyzed for the presence of transmembrane domains coding for putative membrane-bound molecules. Isolated cDNA sequences that have either one or more transmembrane domain(s) within the sequence are provided in SEQ ID NOS: 45-63, 239-253, 359-364, 400-402, 435, 436, 450-452 and

15   455. The cDNA sequences of SEQ ID NOS: 45-48, 239-249, 359-361, 363, 450, 451 and 455 were found to have less than 75% identity (determined as described above) to sequences in the EMBL database, using the FASTA or BLASTN computer algorithms. The amino acid sequences encoded by the cDNA sequences of SEQ ID NO: 45-48, 239-249, 359-361, 363, 450 and 451 (provided in SEQ ID NOS: 164-167,

20   316-326, 383, 385-388, 407-408, 460 and 461, respectively) were found to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the FASTX or BLASTP database. The cDNA sequence of SEQ ID NO: 455 encodes the same amino acid sequence as the cDNA sequence of SEQ ID NO: 359, namely SEQ ID NO: 383.

25   Comparison of the amino acid sequences corresponding to the cDNA sequences of SEQ ID NOS: 49-63, 250-253, 436 and 452 with those in the SwissProt database showed less than 75% identity (determined as described above) to known sequences. These predicted amino acid sequences are provided in SEQ ID NOS: 168-182, 327-330, 457 and 462, respectively.

Using automated search programs to screen against sequences coding for molecules reported to be of therapeutic and/or diagnostic use, some of the cDNA sequences isolated as described above in Example 1 were determined to encode predicted protein sequences that appear to be family members of known protein

5    families. A family member is here defined to have at least 25% identity in the translated polypeptide to a known protein or member of a protein family. These cDNA sequences are provided in SEQ ID NOS: 64-76, 254-264, 365-369, 403, 437-439, 453 and 454. The amino acid sequences encoded by the cDNA sequences of SEQ ID NO: 64-76, 254-264, 365-369, 403, 438, 439 and 453 are provided in SEQ ID

10   NOS: 183-195, 331-341, 389-393, 409, 458, 459 and 463, respectively.

The cDNA sequences of SEQ ID NO: 437 and 454 encode the same amino acid sequences as the cDNA sequences of SEQ ID NO: 68 and 262, namely SEQ ID NO: 187 and 339, respectively. The cDNA sequences of SEQ ID NOS: 64-68, 254-264, 365-369, 453 and 454 show less than 75% identity (determined as described

15   above) to sequences in the EMBL database using the FASTA or BLASTN computer algorithms. Similarly, the amino acid sequences of SEQ ID NOS: 183-195, 331-341, 389-393, 458, 459 and 463 show less than 75% identity to sequences in the SwissProt database.

The utility for each of the proteins encoded by the DNA sequences of SEQ ID

20   NOS: 64-76, 254-264, 365-369, 403, 438, 439, 453 and 454, based on similarity to known proteins, is provided below:

Table 2

FUNCTIONS OF NOVEL PROTEINS

| P/N SEQ ID NO: | A/A SEQ ID NO | SIMILARITY TO KNOWN PROTEINS; FUNCTION |
|---|---|---|
| 64, 372 | 183, 396 | Slit, a secreted molecule required for central nervous system development |
| 65 | 184 | Immunoglobulin receptor family. About 40% of leucocyte membrane polypeptides contain immunoglobulin superfamily domains |
| 66, 403 | 185, 409 | RIP protein kinase, a serine/threonine kinase that contains a death domain to mediate apoptosis |
| 67 | 186 | Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation |
| 68, 437 | 187 | Transforming growth factor alpha, a protein which binds epidermal growth factor receptor and stimulates growth and mobility of keratinocytes |
| 69 | 188 | DRS protein which has a secretion signal component and whose expression is suppressed in cells transformed by oncogenes |
| 70 | 189 | A33 receptor with immunoglobulin-like domains and is expressed in greater than 95% of colon tumors |
| 71 | 190 | Interleukin-12 alpha subunit, component of a cytokine that is important in the immune defense against intracellular pathogens. IL-12 also stimulates proliferation and differentiation of TH1 subset of lymphocytes |
| 72 | 191 | Tumor Necrosis Factor receptor family of proteins that are involved in the proliferation, differentiation and death of many cell types including B and T lymphocytes. |
| 73, 438 | 192, 458 | Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. EGF is involved in wound healing. It also inhibits gastric acid secretion. |
| 74 | 193 | Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors |
| 75, 439 | 194, 459 | Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction |
| 76 | 195 | Immunoglobulin receptor family |
| 254 | 331 | Receptor with immunoglobul in-like domains and homology to A33 receptor which is expressed in greater than 95% of colon tumors |
| 255 | 332 | Epidermal growth factor family proteins which stimulate growth and mobility of keratinocytes and epithelial cells. |

| P/N SEQ ID NO: | A/A SEQ. ID NO: | SIMILARITY TO KNOWN PROTEINS; FUNCTION |
|---|---|---|
| | | EGF is involved in wound healing. It also inhibits gastric acid secretion. |
| 256 | 333 | Serine/threonine kinases (STK2_HUMAN) which participate in cell cycle progression and signal transduction |
| 257 | 334 | Contains protein kinase and ankyrin domains. Possible role in cellular growth and differentiation. |
| 258 | 335 | Notch family proteins which are receptors involved in cellular differentiation. |
| 259 | 336 | Extracellular protein with epidermal growth factor domain capable of stimulating fibroblast proliferation. |
| 260, 453 | 337, 463 | Fibronectin Type III receptor family. The fibronectin III domains are found on the extracellular regions of cytokine receptors. |
| 261 | 338 | Immunoglobulin receptor family |
| 262, 454 | 339 | ADP/ATP transporter family member containing a calcium binding site. |
| 263 | 340 | Mouse CXC chemokine family members are regulators of epithelial, lymphoid, myeloid, stromal and neuronal cell migration and cancers, agents for the healing of cancers, neuro-degenerative diseases, wound healing, inflammatory autoimmune diseases like psoriasis, asthma, Crohns disease and as agents for the prevention of HIV-1 of leukocytes |
| 264 | 341 | Nucleotide-sugar transporter family member. |
| 365 | 389 | Transforming growth factor betas (TGF-betas) are secreted covalently linked to latent TGF-beta-binding proteins (LTBPs). LTBPs are deposited in the extracellular matrix and play a role in cell growth or differentiation. |
| 366 | 390 | Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion. |
| 367 | 391 | Integrins are Type I membrane proteins that function as laminin and collagen receptors and play a role in cell adhesion. |
| 368 | 392 | Cell wall protein precursor. Are involved in cellular growth or differentiation. |
| 369 | 393 | HT protein is a secreted glycoprotein with an EGF-like domain. It functions as a modulator of cell growth, death or differentiation. |

These isolated sequences thus encode proteins that influence the growth, differentiation and activation of several cell types. They may usefully be developed as agents for the treatment and diagnosis of skin wounds, cancers, growth and developmental defects, and inflammatory disease.

5          The polynucleotide sequences of SEQ ID NOS: 77-117, 265-267 and 404-405 are differentially expressed in either keratinocyte stem cells (KSCL) or in transit amplified cells (TRAM) on the basis of the number of times these sequences exclusively appear in either one of the above two libraries; more than 9 times in one and none in the other (Audic S. and Claverie J-M, *Genome Research*, 7:986-995, 10 1997). The sequences of SEQ ID NOS: 77-89, 265-267 and 365-369 were determined to have less than 75% identity to sequences in the EMBL and SwissProt databases using the computer algorithm FASTA or BLASTN, as described above. The proteins encoded by these polynucleotide sequences have utility as markers for identification and isolation of these cell types, and antibodies against these proteins 15 may be usefully employed in the isolation and enrichment of these cells from complex mixtures of cells. Isolated polynucleotides and their corresponding proteins exclusive to the stem cell population can be used as drug targets to cause alterations in regulation of growth and differentiation of skin cells, or in gene targeting to transport specific therapeutic molecules to skin stem cells.

20

## Example 3

### ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF MUTR1

The human homolog of muTR1 (SEQ ID NO: 68), obtained as described above in Example 1, was isolated by screening 50,000 pfu's of an oligo dT primed 25 HeLa cell cDNA library. Plaque lifts, hybridization, and screening were performed using standard molecular biology techniques (Sambrook, J, Fritsch, EF and Maniatis, T, eds., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor: New York, 1989). The determined cDNA sequence of the isolated human homolog (huTR1) is provided in SEQ ID NO: 118, 30 with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 196. The library was screened using an $[\alpha\,^{32}P]$-dCTP labeled double stranded cDNA probe corresponding to nucleotides 1 to 459 of the coding region within SEQ ID NO:

118.

The polypeptide sequence of huTR1 has regions similar to Transforming Growth Factor-alpha, indicating that this protein functions like an epidermal growth factor (EGF). This EGF-like protein will serve to stimulate keratinocyte growth and

5     motility, and to inhibit the growth of epithelial-derived cancer cells. This novel gene and its encoded protein may thus be used as agents for the healing of wounds and regulators of epithelial-derived cancers.

Analysis of RNA transcripts by Northern Blotting

10    Northern analysis to determine the size and distribution of mRNA for huTR1 was performed by probing human tissue mRNA blots (Clontech) with a probe comprising nucleotides 93-673 of SEQ ID NO: 118, radioactively labeled with $[\alpha^{32}P]$-dCTP. Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook, et al., Ibid. mRNA for huTR1 was 3.5-4kb in

15    size and was observed to be most abundant in heart and placenta, with expression at lower levels being observed in spleen, thymus prostate and ovary (Fig. 1).

The high abundance of mRNA for huTR1 in the heart and placenta indicates a role for huTR1 in the formation or maintenance of blood vessels, as heart and placental tissues have an increased abundance of blood vessels, and therefore

20    endothelial cells, compared to other tissues in the body. This, in turn, demonstrates a role for huTR1 in angiogenesis and vascularization of tumors. This is supported by the ability of Transforming Growth Factor-alpha and EGF to induce de novo development of blood vessels (Schreiber, et al., Science 232:1250-1253, 1986) and stimulate DNA synthesis in endothelial cells (Schreiber, et al., Science 232:1250-

25    1253, 1986), and their over-expression in a variety of human tumors.

*Purification of muTR1 and huTR1*

Polynucleotides 177-329 of muTR1 (SEQ ID NO: 268), encoding amino acids 53-103 of muTR1 (SEQ ID NO: 342), and polynucleotides 208-360 of huTR1 (SEQ

30    ID NO: 269), encoding amino acids 54-104 of huTR1 (SEQ ID NO: 343), were cloned into the bacterial expression vector pProEX HT (BRL Life Technologies), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These

27▲

constructs were transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid.*

Starter cultures of these recombinant XL1-Blue *E. coli* were grown overnight at 37°C in Terrific broth containing 100 μg/ml ampicillin. This culture was spun down 5 and used to inoculate 500 ml culture of Terrific broth containing 100 μg/ml ampicillin. Cultures were grown until the $OD_{595}$ of the cells was between 0.4 and 0.8, whereupon IPTG was added to 1 mM. Cells were induced overnight and bacteria were harvested by centrifugation.

Both the polypeptide of muTR1 (SEQ ID NO: 342; referred to as muTR1a) 10 and that of huTR1 (SEQ ID NO: 343; referred to as huTR1a) were expressed in insoluble inclusion bodies. In order to purify the polypeptides muTR1a and huTR1a, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM beta mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP40 was added and the mix incubated on ice for 10 minutes. Lysates were further disrupted by sonication 15 on ice at 95W for 4 x 15 seconds and then centrifuged for 15 minutes at 14,000 rpm to pellet the inclusion bodies.

The resulting pellet was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated on ice for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14,000 rpm for 15 minutes at 4 °C and the supernatant discarded. The 20 pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M Guanidine HCl, 0.5 M NaCl, 20 mM Tris HCl, pH 8.0), sonicated at 95 W for 4 x 15 seconds and then centrifuged for 20 minutes at 14,000 rpm and 4 °C to remove debris. The supernatant was stored at 4 °C until use.

25 Polypeptides muTR1a and huTR1a were purified by virtue of the N-terminal 6x Histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating Sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's recommended protocol. In order to refold the proteins once purified, the protein solution was added to 5x its volume of refolding buffer (1 mM 30 EDTA, 1.25 mM reduced glutathione, 0.25 mM oxidised glutathione, 20 mM Tris-HCl, pH 8.0) over a period of 1 hour at 4 °C. The refolding buffer was stirred rapidly

during this time, and stirring continued at 4 °C overnight. The refolded proteins were then concentrated by ultrafiltration using standard protocols.

### *Biological Activities of Polypeptides muTR1a and huTR1a*

5        muTR1 and huTR1 are novel members of the EGF family, which includes EGF, TGFα, epiregulin and others. These growth factors are known to act as ligands for the EGF receptor. The pathway of EGF receptor activation is well documented. Upon binding of a ligand to the EGF receptor, a cascade of events follows, including the phosphorylation of proteins known as MAP kinases. The phosphorylation of

10      MAP kinase can thus be used as a marker of EGF receptor activation. Monoclonal antibodies exist which recognize the phosphorylated forms of 2 MAP kinase proteins – ERK1 and ERK2.

         In order to examine whether purified polypeptides of muTR1a and huTR1a act as a ligand for the EGF receptor, cells from the human epidermal carcinoma cell line

15      A431 (American Type Culture Collection, No. CRL-1555, Manassas, Virginia) were seeded into 6 well plates, serum starved for 24 hours, and then stimulated with purified muTR1a or huTR1a for 5 minutes in serum free conditions. As a positive control, cells were stimulated in the same way with 10 to 100 ng/ml TGF-alpha or EGF. As a negative control, cells were stimulated with PBS containing varying

20      amounts of LPS. Cells were immediately lysed and protein concentration of the lysates estimated by Bradford assay. 15 µg of protein from each sample was loaded onto 12% SDS-PAGE gels. The proteins were then transferred to PVDF membrane using standard techniques.

         For Western blotting, membranes were incubated in blocking buffer (10mM

25      Tris-HCl, pH 7.6, 100 mM NaCl, 0.1% Tween-20, 5% non-fat milk) for 1 hour at room temperature. Rabbit anti-Active MAP kinase pAb (Promega, Madison, Wisconsin) was added to 50 ng/ml in blocking buffer and incubated overnight at 4 °C. Membranes were washed for 30 mins in blocking buffer minus non-fat milk before being incubated with anti rabbit IgG-HRP antibody, at a 1:3500 dilution in blocking

30      buffer, for 1 hour at room temperature. Membranes were washed for 30 minutes in blocking buffer minus non-fat milk, then once for 5 minutes in blocking buffer minus

non-fat milk and 0.1% Tween-20. Membranes were then exposed to ECL reagents for 2 min, and then autoradiographed for 5 to 30 min.

As shown in Fig. 2, both muTR1a and huTR1a were found to induce the phosphorylation of ERK1 and ERK2 over background levels, indicating that muTR1
5    and huTR1 act as ligands for a cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor. As shown in Fig. 11, huTR1a was also demonstrated to induce the phosphorylation of ERK1 and ERK2 in CV1/EBNA kidney epithelial cells in culture, as compared with the negative control. These assays were conducted as described above. This indicates that huTR1a acts as a ligand for a
10   cell surface receptor that activates the MAP kinase signaling pathway, possibly the EGF receptor in HeLa and CV1/EBNA cells.

The ability of muTR1a to stimulate the growth of neonatal foreskin (NF) keratinocytes was determined as follows. NF keratinocytes derived from surgical discards were cultured in KSFM (BRL Life Technologies) supplemented with bovine
15   pituatary extract (BPE) and epidermal growth factor (EGF). The assay was performed in 96 well flat-bottomed plates in 0.1 ml unsupplemented KSFM. MuTR1a, human transforming growth factor alpha (huTGFα) or PBS-BSA was titrated into the plates and $1 \times 10^3$ NF keratinocytes were added to each well. The plates were incubated for 5 days in an atmosphere of 5% $CO_2$ at $37^0C$. The degree of
20   cell growth was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 3, both muTR1a and the positive control human TGFα stimulated the growth of NF keratinocytes, whereas the negative control, PBS-BSA, did not.

The ability of muTR1a and huTR1a to stimulate the growth of a transformed
25   human keratinocyte cell line, HaCaT, was determined as follows. The assay was performed in 96 well flat-bottomed plates in 0.1 ml DMEM (BRL Life Technologies) supplemented with 0.2% FCS. MuTR1a, huTR1a and PBS-BSA were titrated into the plates and $1 \times 10^3$ HaCaT cells were added to each well. The plates were incubated for 5 days in an atmosphere containing 10% $CO_2$ at $37^0C$. The degree of cell growth
30   was determined by MTT dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown in Fig. 4, both muTR1a and huTR1a stimulated the growth of HaCaT cells, whereas the negative control PBS-BSA did not.

The ability of muTR1a and huTR1a to inhibit the growth of A431 cells was determined as follows. Polypeptides muTR1a (SEQ ID NO: 342) and huTR1a (SEQ ID NO: 343) and PBS-BSA were titrated as described previously (*J. Cell. Biol.* 93:1-4, 1982), and cell death was determined using the MTT dye reduction as described

5   previously (*J. Imm. Meth.* 93:157-165, 1986). Both muTR1a and huTR1a were found to inhibit the growth of A431 cells, whereas the negative control PBS-BSA did not (Fig. 5).

These results indicate that muTR1 and huTR1 stimulate keratinocyte growth and motility, inhibit the growth of epithelial-derived cancer cells, and play a role in

10  angiogenesis and vascularization of tumors. This novel gene and its encoded protein may thus be developed as agents for the healing of wounds, angiogenesis and regulators of epithelial-derived cancers.


## *Upregulation of huTR1 and mRNA expression*

15  HeLa cells (human cervical adenocarcinoma) were seeded in 10 cm dishes at a concentration of $1 \times 10^6$ cells per dish. After incubation overnight, media was removed and replaced with media containing 100 ng/ml of muTR1, huTR1, huTGFα, or PBS as a negative control. After 18 hours, media was removed and the cells lysed in 2 ml of TRIzol reagent (Gibco BRL Life Technologies, Gaithersburg, Maryland).

20  Total RNA was isolated according to the manufacturer's instructions. To identify mRNA levels of huTR1 from the cDNA samples, 1 μl of cDNA was used in a standard PCR reaction. After cycling for 30 cycles, 5 μl of each PCR reaction was removed and separated on a 1.5% agarose gel. Bands were visualized by ethidium bromide staining. As can be seen from Fig. 12, both mouse and human TR1 up-

25  regulate the mRNA levels of huTR1 as compared with cells stimulated with the negative control of PBS. Furthermore, TGFα can also up-regulate the mRNA levels of huTR1.

These results indicate that TR1 is able to sustain its own mRNA expression and subsequent protein expression, and thus is expected to be able to contribute to the

30  progression of diseases such as psoriasis where high levels of cytokine expression are involved in the pathology of the disease. Furthermore, since TGFα can up-regulate

the expression of huTR1, the up-regulation of TR1 mRNA may be critical to the mode of action of TGFα.

*Serum response element reporter gene assay*

5    The serum response element (SRE) is a promoter element required for the regulation of many cellular immediate-early genes by growth. Studies have demonstrated that the activity of the SRE can be regulated by the MAP kinase signaling pathway. Two cell lines, PC12 (rat pheochromocytoma – neural tumor) and HaCaT (human transformed keratinocytes), containing eight SRE upstream of an

10   SV40 promotor and luciferase reporter gene were developed in-house. $5 \times 10^3$ cells were aliquoted per well of 96 well plate and grown for 24 hours in their respective media. HaCaT SRE cells were grown in 5% fetal bovine serum (FBS) in D-MEM supplemented with 2mM L-glutamine (Sigma, St. Louis, Missouri), 1mM sodium pyruvate (BRL Life Technologies), 0.77mM L-asparagine (Sigma), 0.2mM arginine

15   (Sigma), 160mM penicillin G (Sigma), 70mM dihydrostreptomycin (Roche Molecular Biochemicals, Basel, Switzerland), and 0.5 mg/ml geneticin (BRL Life Technologies). PC12 SRE cells were grown in 5% fetal bovine serum in Ham F12 media supplemented with 0.4 mg/ml geneticin (BRL Life Technologies). Media was then changed to 0.1% FBS and incubated for a further 24 hours. Cells were then

20   stimulated with a titration of TR1 from 1 µg/ml. A single dose of basic fibroblast growth factor at 100 ng/ml (R&D Systems, Minneapolis, Minnesota) or epidermal growth factor at 10 ng/ml (BRL Life Technologies) was used as a positive control. Cells were incubated in the presence of muTR1 or positive control for 6 hours, washed twice in PBS and lysed with 40 µl of lysis buffer (Promega). 10 µl was

25   transferred to a 96 well plate and 10 µl of luciferase substrate (Promega) added by direct injection into each well by a Victor$^2$ fluorimeter (Wallac), the plate was shaken and the luminescence for each well read at 3x1 sec Intervals. Fold induction of SRE was calculated using the following equation: Fold induction of SRE = Mean relative luminescence of agonist/Mean relative luminescence of negative control.

30   As shown in Fig. 13, muTR1 activated the SRE in both PC-12 (Fig. 13A) and HaCaT (Fig. 13B) cells. This indicates that HaCaT and PC-12 cells are able to respond to muTR1 protein and elicit a response. In the case of HaCaT cells, this is a

growth response.   In the case of PC-12 cells, this may be a growth, a growth inhibition, differentiation, or migration response.   Thus, TR1 may be important in the development of neural cells or their differentiation into specific neural subsets.   TR1 may also be important in the development and progression of neural tumors.

5

*Inhibition by the EGF receptor assay*

The HaCaT growth assay was conducted as previously described, with the following modifications.   Concurrently with the addition of EGF and TR1 to the media, anti-EGF Receptor (EGFR) antibody (Promega, Madison, Wisconsin) or the

10    negative control antibody, mouse IgG (PharMingen, San Diego, California), were added at a concentration of 62.5 ng/ml.

As seen in Fig. 14, an antibody which blocks the function of the EGFR inhibited the mitogenicity of TR1 on HaCaT cells.  This indicates that the EGFR is crucial for transmission of the TR1 mitogenic signal on HaCaT cells.  TR1 may bind

15    directly to the EGF receptor.  TR1 may also bind to any other members of the EGFR family (for example, ErbB-2, -3, and/or -4) that are capable of heterodimerizing with the EGFR.

*Splice variants of huTR1*

A variant of huTR1 was isolated from the same library as huTR1, following the same protocols. The sequence referred to as huTR1-1 (also known as TR1δ) is a splice variant of huTR1 and consists of the ORF of huTR1 minus amino acids 15 to

5    44 and 87 to 137. These deletions have the effect of deleting part of the signal sequence and following amino terminal linker sequence, residues following the second cysteine residue of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, huTR1-1

10   is an intracellular form of huTR1. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGFα. The determined nucleotide sequence of huTR1-1, is given in SEQ ID NO: 412, with the corresponding amino acid sequence being provided in SEQ ID NO: 415.

Four additional splice variants of huTr1 were isolated by PCR on first strand

15   cDNA made from RNA isolated from HeLa cells by standard protocols. These splice variants of huTR1 are referred to as TR1-2 (also known as TR1β), TR1-3 (also known as TR1γ), TR1ε and TR1φ.

TR1-2 consists of the ORF of huTR1 minus amino acids 95 to 137. This deletion has the effect of deleting the transmembrane domain. Therefore TR1-2 is a

20   secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGFα. The determined cDNA sequence of TR1-2 is given in SEQ ID NO: 410 and the corresponding amino acid sequence in SEQ ID NO: 413.

25   TR1-3 consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 86 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence, residues following the second cysteine of the EGF motif and the following transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely

30   not affected. Therefore, TR1-3 is also a secreted form of huTR1 and functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and

TGFα. The determined cDNA sequence of TR1-3 is given in SEQ ID NO: 411 and the corresponding amino acid sequence is SEQ ID NO: 414.

TR1ε consists of the ORF of huTR1 minus amino acids 86 to 136. This deletion has the effect of deleting residues following the second cysteine of the EGF

5    motif and the transmembrane domain. However, cysteine residue 147 (huTR1 ORF numbering) may replace the deleted cysteine and thus the disulphide bridges are likely not affected. Therefore, TR1ε is also a secreted form of huTR1 and functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGFα. The determined cDNA sequence of TR1ε is given in SEQ ID NO: 371 and the

10   corresponding predicted amino acid sequence in SEQ ID NO: 395.

TR1φ consists of the ORF of huTR1 minus amino acids 36 to 44 and amino acids 95 to 136. These deletions have the effect of deleting part of the amino terminal linker sequence and the transmembrane domain. Therefore TR1φ is a secreted form of huTR1 and binds with equal or greater affinity to the TR1 receptor as huTR1, since

15   the EGF domain remains intact. It functions as an agonist or an antagonist to huTR1 or other EGF family members, including EGF and TGFα. The determined nucleotide sequence of TR1φ is given in SEQ ID NO: 416 and the corresponding predicted amino acid sequence in SEQ ID NO: 417.


20                                      Example 4

IDENTIFICATION, ISOLATION AND CHARACTERIZATION OF DP3

A partial cDNA fragment, referred to as DP3, was identified by differential display RT-PCR (modified from Liang P and Pardee AB, *Science* 257:967-971, 1992) using mRNA from cultured rat dermal papilla and footpad fibroblast cells, isolated by

25   standard cell biology techniques. This double stranded cDNA was labeled with [α$^{32}$P]- dCTP and used to identify a full length DP3 clone by screening 400,000 pfu's of an oligo dT-primed rat dermal papilla cDNA library. The determined full-length cDNA sequence for DP3 is provided in SEQ ID NO: 119, with the corresponding amino acid sequence being provided in SEQ ID NO: 197. Plaque lifts, hybridization

30   and screening were performed using standard molecular biology techniques.

## Example 5
## ISOLATION AND CHARACTERIZATION OF KS1

### *Analysis of RNA transcripts by Northern Blotting*

5        Northern analysis to determine the size and distribution of mRNA for muKS1 (SEQ ID NO: 263) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with $[\alpha^{32}P]$-dCTP. Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al., Ibid.*   mRNA for muKS1 was 1.6 kb in size and was

10      observed to be most abundant in brain, lung, or any muscle, and heart. Expression could also be detected in lower intestine, skin, bone marrow, and kidney.  No detectable signal was found in testis, spleen, liver, thymus, stomach.

### *Human homologue of muKS1*

        MuKS1 (SEQ ID NO: 263) was used to search the EMBL database (Release

15      50, plus updates to June, 1998) to identify human EST homologues.  The top three homologies were to the following ESTs: accession numbers AA643952, HS1301003 and AA865643.  These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively.  Frame shifts were identified in AA643952 and HS1301003 when translated.  Combination of all three

20      ESTs identified huKS1 (SEQ ID NO: 270) and translated polypeptide SEQ ID NO: 344.  Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

### *Identification of KSCL009274 cDNA sequence*

25        A directionally cloned cDNA library was constructed from immature murine keratinocytes and submitted for high-throughput sequencing.  Sequence data from a clone designated KDCL009274 showed 35% identity over 72 amino acids with rat macrophage inflammatory protein-2B (MIP-2B) and 32% identity over 72 amino acids with its murine homologue.  The insert of 1633bp (SEQ ID NO: 464; Fig. 15A)

30      contained an open reading frame of 300bp with a 5' untranslated region of 202bp and a 3' untranslated region of 1161bp.  A poly-adenylation signal of AATAAA is present 19 base pairs upstream of the poly-A tail.  The predicted mature polypeptide (SEQ ID

NO: 465) is 77 amino acids in length containing 4 conserved cysteines with no ELR

motif. The putative signal peptide cleavage site beween GLY 22 and Ser 23 was

predicted by the hydrophobicity profile. This putative chemokine was identical to

KS1. The full length sequence was screened against the EMBL database using the

5    BLAST program and showed some identity at the nucleotide level with human EST

clones AA643952, AA865643, and HS1301003, respectively. A recently described

human CXC chemokine, BRAK, has some identity with KS1 at the protein level. The

alignment of KS1 (referred to in Fig. 15B as KLF-1), BRAK, and other murine

α-chemokines is shown in Fig. 15B. The phylogenetic relationship between KS1 and

10   other α-chemokine family members was determiend using the Phylip program. KS1

and BRAK demonstrate a high degree of divergence from the other α-chemokines,

supporting the relatively low homology shown in the multiple alignment.

_Bacterial expression and purification of muKS1 and huKS1_

15        Polynucleotides 269-502 of muKS1 (SEQ ID NO: 271), encoding amino acids

23-99 of polypeptide muKS1 (SEQ ID NO: 345), and polynucleotides 55-288 of

huKS1 (SEQ ID NO: 272), encoding amino acids 19-95 of polypeptide huKS1 (SEQ

ID NO: 346), were cloned into the bacterial expression vector pET-16b (Novagen,

Madison, Wisconsin), which contains a bacterial leader sequence and N-terminal

20   6xHistidine tag. These constructs were transformed into competent XL1-Blue _E. coli_

as described in Sambrook et al., _Ibid_.

Starter cultures of recombinant BL 21 (DE3) _E. coli_ (Novagen) containing

SEQ ID NO: 271 (muKS1a) and SEQ ID NO: 272 (huKS1a) were grown in NZY

broth containing 100 μg/ml ampicillin (Gibco-BRL Life Technologies) at 37°C.

25   Cultures were spun down and used to inoculate 800 ml of NZY broth and 100 μg/ml

ampicillin. Cultures were grown until the $OD_{595}$ of the cells was between 0.4 and 0.8.

Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression

produced an induced band of approximately 15kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order

30   to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20

mM Tris-HCl pH 8.0, 10 mM βMercaptoethanol, 1 mM PMSF). To the lysed cells,

1% NP-40 was added and the mix incubated on ice for 10 minutes. Lysates were

further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on

5    ice for 1 hour, centrifuged at 14000 rpm for 15 minutes at 4°C and the supernatant discarded. The pellet was once more re-suspended in lysis buffer containing 0.5% w/v CHAPS, sonicated, centrifuged, and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95W for 4 x 15 seconds and centrifuged for 10 minutes

10   at 18000 rpm and 4°C to remove debris. The supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In

15   order to re-fold the proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM tris-HCl pH 7.5.+ 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 + 10% (w/v) glycerol.  Preparations obtained were greater than 95% pure as determined by SDS-PAGE.  Endotoxin contamination of purified proteins were determined using a

20   limulus amebocyte lysate assay kit (BIO Whittaker, Walkersville, MD).  Endotoxin levels were <0.1 ng/µg of protein.  Internal amino acid sequencing was performed on tryptic peptides of KS1.

An Fc fusion protein was produced by expression in HEK 293 T cells.  35µg of KLF-1pIGFc DNA to transfect 6 x 10$^6$ cells per flask, 200 mls of Fc containing

25   supernatant was produced.  The Fc fusion protein was isolated by chromatography using an Affiprep protein A resin (0.3 ml column, Biorad).  After loading, the column was washed with 15 mls of PBS, followed by a 5 ml wash of 50 mM Na citrate pH 5.0.  The protein was then eluted with 6 column volumes of 50 mM Na citrate pH 2.5, collecting 0.3 ml fractions in tubes containing 60µl of 2M Tris-HCl pH 8.0.  Fractions

30   were analyzed by SDS-PAGE.

*Peptide sequencing of muKS1 and huKS1*

Bacterially expressed muKS1 and huKS1 were separated on polyacrylamide gels and induced bands of 15 kDa were identified. The predicted size of muKS1 is 9.4 kDa. To obtain the amino acid sequence of the 15 kDa bands, 20 μg recombinant muKS1 and huSK1 was resolved by SDS-PAGE and electroblotted onto Immobilon

5    PVDF membrane (Millipore, Bedford, Massachusetts). Internal amino acid sequencing was performed on tryptic peptides of muKS1 and huKS1 by the Protein Sequencing Unit at the University of Auckland, New Zealand.

The determined amino acid sequences for muKS1 and huKS1 are given in SEQ ID NOS: 397 and 398, respectively. These amino acid sequences confirmed that

10   the determined sequences are identical to those predicted from the cDNA sequences. The size discrepancy has previously been reported for other chemokines (Richmond A, Balentien E, Thomas HG, Flaggs G, Barton DE, Spiess J, Bordoni R, Francke U, Derynck R, "Molecular characterization and chromosomal mapping of melanoma growth stimulatory activity, a growth factor structurally related to beta-

15   thromboglobulin," *EMBO J.* 7:2025-2033, 1988; Liao F, Rabin RL, Yannelli JR, Koniaris LG, Vanguri P, Farber JM, "Human Nig chemokine: biochemical and functional characterization," *J. Exp. Med.* 182:1301-1314, 1995). The isoelectric focusing point of these proteins was predicted to be 10.26 using DNASIS (HITACHI Software Engineering, San Francisco, California). Recombinant Fc tagged KS1

20   expresssed and purified using protein A affinity column chromatography revealed a homogenous protein with a molecular mass of 42kDa.

_Oxidative burst assay_

Oxidative burst assays were used to determine responding cell types. $1 \times 10^7$
PBMC cells were resuspended in 5 ml HBSS, 20mM HEPES, 0.5% BSA and
incubated for 30 minutes at 37°C with 5 µl 5 mM dichloro-dihydrofluorescein

5    diacetate (H₂DCFDA, Molecular Probes, Eugene, Oregon). $2 \times 10^5$ H₂DCFDA-
labeled cells were loaded in each well of a flat-bottomed 96 well plate. 10 µl of each
agonist was added simultaneously into the well of the flat-bottomed plate to give final
concentrations of 100 ng/ml (fMLP was used at 10 µM). The plate was then read on a
Victor$^2$ 1420 multilabel counter (Wallac, Turku, Finland) with a 485 nm excitation

10   wavelength and 535 nm emission wavelength. Relative fluorescence was measured at
5 minute intervals over 60 minutes.

A pronounced respiratory burst was identified in PBMC with a 2.5 fold
difference between control treated cells (TR1) and cells treated with 100 ng/ml
muKS1 (Fig. 8). Human stromal derived factor-1α (SDF1α) (100 ng/ml) and 10 µM

15   formyl-Met-Leu-Phe (fMLP) were used as positive controls.


_Chemotaxis assay_

Cell migration in response to muKS1 was tested using a 48 well Boyden's
chamber (Neuro Probe Inc., Cabin John, Maryland) as described in the manufacturer's

20   protocol. In brief, agonists were diluted in HBSS, 20mM HEPES, 0.5% BSA and
added to the bottom wells of the chemotactic chamber. THP-1 cells were re-
suspended in the same buffer at $3 \times 10^5$ cells per 50 µl. Top and bottom wells were
separated by a PVP-free polycarbonate filter with a 5 µm pore size for monocytes or
3 µm pore size for lymphocytes. Cells were added to the top well and the chamber

25   incubated for 2 hours for monocytes and 4 hours for lymphocytes in a 5% CO₂
humidified incubator at 37°C. After incubation, the filter was fixed and cells scraped
from the upper surface. The filter was then stained with Diff-Quick (Dade
International Inc., Miami, Florida) and the number of migrating cells counted in five
randomly selected high power fields. The results are expressed as a migration index

30   (the number of test migrated cells divided by the number of control migrated cells).

Using this assay, muKS1 was tested against T cells and THP-1 cells. MuKS1 induced a titrateable chemotactic effect on THP-1 cells from 0.01 ng/ml to 100 ng/ml (Fig. 9). Human SDF1α was used as a positive control and gave an equivalent migration. MuKS1 was also tested against IL-2 activated T cells. However, no

5     migration was evidence for muKS1 even at high concentrations, whereas SDF-1α provided an obvious titrateable chemotactic stimulus. Therefore, muKS1 appears to be chemotactic for THP-1 cells but not for IL-2 activated T cells at the concentrations tested.

*Flow cytometric binding studies*

10    Binding of KLF-1 to THP-1 and Jurkat cells was tested in the following manner. THP-1 or Jurkat cells ($5 \times 10^6$) were resuspended in 3 mls of wash buffer (2% FBS and 0.2% sodium azide in PBS) and pelleted at 4°C, 200g for 5 minutes. Cells were then blocked with 0.5% mouse and goat sera for 30 minutes on ice. Cells were washed, pelleted, resuspended in 50μl of KLF-1Fc at 10μg/ml and incubated for

15    30 minutes on ice. After incubation, the cells were prepared as before and resuspended in 50μl of goat anti-human IgG biotin (Southern Biotechnology Associates, AL) at 10μg/ml and incuated for 30 minutes on ice. Finally, cells were washed, pelleted and resuspended in 50μl of streptavidin-RPE (Southern Biotechnology Associates, AL) at 10μg/ml and incuabated for a further 30 minutes on

20    ice in the dark. Cells were washed and resuspended in 250μl of wash buffer and stained with 1μl of 10μg/ml propidium iodide (Sigma) to exclude any dead cells. Purified Fc fragment (10μg/ml) was used as a negative control in place of KLF-1Fc to determine non-specific binding. Ten thousand gated events were analyzed on log scale using PE filter arrangement with peak transmittance at 575nm and bandwidth of

25    10nm on an Elite cell sorter (Coulter Cytometry).

The respiratory burst and migration assays indicated that KS1 is active on monocytes and not T cells; therefore, the KS1 Fc fusion protein was tested in a binding study with THP-1 and Jurkat T cells. KS1 Fc showed a marked positive shift on THP-1 cells compared with the Fc fragment alone. In contrast, KS1 demonstrated

30    no positive binding with Jurkat cells in an identical experiment.

*Full length sequence of muKS1 clone*

The nucleotide sequence of muKS1 was extended by determining the base sequence of additional ESTs. Combination of all the ESTs identified the full-length muKS1 (SEQ ID NO: 370) and the corresponding translated polypeptide sequence in

5      SEQ ID NO: 394.


*Analysis of human RNA transcripts by Northern blotting*

Northern blot analysis to determine the size and distribution of mRNA for the human homologue of muKS1 was performed by probing human tissue blots

10     (Clontech, Palo Alto, California) with a radioactively labeled probe consisting of nucleotides 1 to 288 of huKS1 (SEQ ID NO: 270). Prehybridization, hybridization, washing, and probe labeling were performed as described in Sambrook, *et al., Ibid.* mRNA for huKS1 was 1.6 kb in size and was observed to be most abundance in kidney, liver, colon, small intestine, and spleen. Expression could also be detected in

15     pancreas, skeletal muscle, placenta, brain, heart, prostate, and thymus. No detectable signal was found in lung, ovary, and testis.


*Analysis of human RNA transcripts in tumor tissue by Northern blotting*

Northern blot analysis to determine distribution of huKS1 in cancer tissue was

20     performed as described previously by probing tumor panel blots (Invitrogen, Carlsbad, California). These blots make a direct comparison between normal and tumor tissue. MRNA was observed in normal uterine and cervical tissue but not in the respective tumor tissue. In contrast, expression was up-regulated in breast tumor and down-regulated in normal breast tissue. No detectable signal was found in either

25     ovary or ovarian tumors.


*Injection of bacterially recombinant muKS1 into C3H/HeJ mice*

Eighteen C3H/HeJ mice were divided into 3 groups and injected intraperitoneally with muKS1, GV14B, or phosphate buffered saline (PBS). GV14B

30     is a bacterially expressed recombinant protein used as a negative control. Group 1 mice were injected with 50 µg of muKS1 in 1 ml of PBS; Group 2 mice were injected with 50 µg of GV14B in 1 ml of PBS; and Group 3 mice with 1 ml of PBS. After 18

hours, the cells in the peritoneal cavity of the mice were isolated by intraperitoneal lavage with 2 x 4 ml washes with harvest solution (0.02% EDTA in PBS). Viable cells were counted from individual mice from each group. Mice injected with 50 μg of muKS1 had on average a 3-fold increase in cell numbers (Fig. 10).

5          20 μg of bacterial recombinant muKS1 was injected subcutaneously into the left hind foot of three C3H/HeJ mice. The same volume of PBS was injected into the same site on the right-hand side of the same animal. After 18 hours, mice were examined for inflammation. All mice showed a red swelling in the foot pad injected with bacterially recombinant KS1. From histology, sites injected with muKS1 had an

10    inflammatory response of a mixed phenotype with mononuclear and polymorphonuclear cells present.

### Injection of bacterially expressed muKS1a into nude mice

To determine whether T cells are required for the inflammatory response, the

15    experiment was repeated using nude mice. Two nude mice were anaesthetised intraperitoneally with 75 μl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20ug of bacterially expressed muKS1a (SEQ ID NO: 345) was injected subcutaneously in the left hind foot, ear and left-hand side of the back. The same volume of phosphate buffered

20    saline was injected in the same sites but on the right-hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline.

25    Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

30    ### Discussion

Chemokines are a large superfamily of highly basic secreted proteins with a broad number of functions (Baggiolini, et al., Annu. Rev. Immunol., 15:675-705,

1997; Ward, *et al.*, *Immunity*, 9:1-11, 1998; Horuk, *Nature*, 393:524-525, 1998). The polypeptide sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore

5     be expected to stimulate leukocyte, epithelial, stromal, and neuronal cell migration; promote angiogenesis and vascular development; promote neuronal patterning, hemopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes; and promotion of migration in wound healing events. It has recently been shown that receptors to

10    chemokines act as co-receptors for HIV-1 infection of CD4+ cells (Cairns, *et al.*, *Nature Medicine*, 4:563-568, 1998) and that high circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury, *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid,

15    stromal, and neuronal cells migration and cancers; as agents for the treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases such as psoriasis, asthma and Crohn's disease for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

We have also shown that muKS1 promotes a quantifiable increase in cell

20    numbers in the peritoneal cavity of C3H/HeJ mice injected with muKS1. Furthermore, we have shown that muKS1 induces an oxidative burst in human peripheral blood mononuclear cells and migration in the human monocyte leukemia cell line, THP-1, suggesting that monocyte/macrophages are one of the responsive cell types for KS1. In addition to this, we demonstrated that huKS1 was expressed at

25    high levels in a number of non-lymphoid tissues, such as the colon and small intestine, and in breast tumors. It was also expressed in normal uterine and cervical tissue, but was completely down-regulated in their respective tumors. It has recently been shown that non-ELR chemokines have demonstrated angiostatic properties. IP-10 and Mig, two non-ELR chemokines, have previously been shown to be up-

30    regulated during regression of tumors (Tannenbaum CS, Tubbs R, Armstrong D, Finke JH, Bukowski RM, Hamilton TA, "The CXC Chemokines IP-10 and Mig are necessary for IL-12-mediated regression of the mouse RENCA tumor," *J. Immunol.*

161: 927-932, 1998), with levels of expression inversely correlating with tumor size (Kanegane C, Sgadari C, Kanegane H, Teruya-Feldstine J, Yao O, Gupta G, Farber JM, Liao F, Liu L, Tosato G, "Contribution of the CXC Chemokines IP-10 and Mig to the antitumor effects of IL-12," *J. Leuko. Biol.* 64: 384-392, 1998). Furthermore, neutralizing antibodies to IP-10 and Mig would reduce the anti-tumor effect, indicating the contribution these molecules make to the anti-tumor effects. Therefore, it is expected that in the case of cervical and uterine tumors, KS1 would have similar properties.

The data demonstrates that KS1 is involved in cell migration showing that one of the responsive cell types is monocyte/macrophage. The human expression data in conjunction with the *in vitro* and *in vivo* biology demonstrates that this molecule may be a useful regulator in cell migration, and as an agent for the treatment of inflammatory diseases, such as Crohn's disease, ulcerative colitis, and rheumatoid arthritis; and cancers, such as cervical adenocarcinoma, uterine leiomyoma, and breast invasive ductal carcinoma.

## Example 6

### CHARACTERIZATION OF KS2

KS2 contains a transmembrane domain and may function as either a membrane-bound ligand or a receptor. Northern analysis indicated that the mRNA for KS2 was expressed in the mouse keratinocyte cell line, Pam212, consistent with the cDNA being identified in mouse keratinocytes.

*Mammalian Expression*

To express KS2, the extracellular domain was fused to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This was performed by cloning polynucleotides 20-664 of KS2 (SEQ ID NO: 273), encoding amino acids 1-215 of polypeptide KS2 (SEQ ID NO: 347), into the mammalian expression vector pcDNA3 (Invitrogen, NV Leek, Netherlands), to the amino terminus of the constant domain of immunoglobulinG (Fc) that had a C-terminal 6xHistidine tag. This construct was transformed into competent XL1-Blue *E. coli* as described in Sambrook et al., *Ibid.* The Fc fusion construct of KS2a was expressed by transfecting Cos-1 cells in 5 x T175 flasks with 180 µg of KS1a using

DEAE-dextran. The supernatant was harvested after seven days and passed over a Ni-NTA column. Bound KS2a was eluted from the column and dialysed against PBS.

The ability of the Fc fusion polypeptide of KS2a to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes was determined as follows.

5    A single cell suspension was prepared from the spleens of BALB/c mice and washed into DMEM (GIBCO-BRL) supplemented with 2 mM L-glutamine, 1 mM sodium pyruvate, 0.77 mM L-asparagine, 0.2 mM L-arganine, 160 mM penicillin G, 70 mM dihydrostreptomycin sulfate, $5 \times 10^{-2}$ mM beta mercaptoethanol and 5% FCS (cDMEM). Splenocytes ($4 \times 10^6$/ml) were stimulated with 2 ug/ml concanavalin A

10   for 24 hrs at 37°C in 10% $CO_2$. The cells were harvested from the culture, washed 3 times in cDMEM and resuspended in cDMEM supplemented with 10 ng/ml rhuIL-2 at $1 \times 10^5$ cells/ml. The assay was performed in 96 well round bottomed plates in 0.2 ml cDMEM. The Fc fusion polypeptide of KS2a, PBS, LPS and BSA were titrated into the plates and $1 \times 10^4$ activated T cells (0.1 ml) were added to each well. The

15   plates were incubated for 2 days in an atmosphere containing 10% $CO_2$ at $37^0$C. The degree of proliferation was determined by pulsing the cells with 0.25 uCi/ml tritiated thymidine for the final 4 hrs of culture after which the cells were harvested onto glass fiber filtermats and the degree of thymidine incorporation determined by standard liquid scintillation techniques. As shown in Fig. 6, the Fc fusion polypeptide of KS2a

20   was found to inhibit the IL-2 induced growth of concanavalin A stimulated murine splenocytes, whereas the negative controls PBS, BSA and LPS did not.

This data demonstrates that KS2 is expressed in skin keratinocytes and inhibits the growth of cytokine induced splenocytes. This suggests a role for KS2 in the regulation of skin inflammation and malignancy.

25

## Example 7

### Characterization of KS3

KS3 encodes a polypeptide of 40 amino acids (SEQ ID NO: 129). KS3 contains a signal sequence of 23 amino acids that would result in a mature

30   polypeptide of 17 amino acids (SEQ ID NO: 348; referred to as KS3a).

KS3a was prepared synthetically (Chiron Technologies, Victoria, Australia) and observed to enhance transferrin-induced growth of the rat intestinal epithelial

cells IEC-18 cells. The assay was performed in 96 well flat-bottomed plates in 0.1 ml
DMEM (GIBCO-BRL Life Technologies) supplemented with 0.2% FCS. KS3a (SEQ
ID NO: 348), apo-Transferrin, media and PBS-BSA were titrated either alone, with
750 ng/ml Apo-transferrin or with 750 ng/ml BSA, into the plates and $1 \times 10^3$ IEC-18
5      cells were added to each well. The plates were incubated for 5 days at $37^0C$ in an
atmosphere containing 10% $CO_2$. The degree of cell growth was determined by MTT
dye reduction as described previously (*J. Imm. Meth.* 93:157-165, 1986). As shown
in Fig. 7, KS3a plus Apo-transferrin was found to enhance transferrin-induced growth
of IEC-18 cells, whereas KS3a alone or PBS-BSA did not, indicating that KS3a and
10     Apo-transferrin act synergistically to induce the growth of IEC-18 cells.

This data indicates that KS3 is epithelial derived and stimulates the growth of
epithelial cells of the intestine. This suggests a role for KS3 in wound healing,
protection from radiation- or drug-induced intestinal disease, and integrity of the
epithelium of the intestine.

15     SEQ ID NOS: 1-465 are set out in the attached Sequence Listing. The codes
for polynucleotide and polypeptide sequences used in the attached Sequence Listing
confirm to WIPO Standard ST.25 (1988), Appendix 2.

All references cited herein, including patent references and non-patent
references, are hereby incorporated by reference in their entireties.

20     Although the present invention has been described in terms of specific
embodiments, changes and modifications can be carried out without departing from
the scope of the invention which is intended to be limited only by the scope of the
appended claims.

## We claim:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (b) complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (c) reverse complements of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (d) reverse sequences of the sequences recited in SEQ ID NOS: 1-119, 198-276, 349-372, 399-405, 410-412, 416, 418-455 and 464; (e) sequences having at least a 99% probability of being the same as a sequence selected from any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters described above; and (f) nucleotide sequences having at least 50% identity to any of the sequences in (a)-(d), above, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

2. An expression vector comprising an isolated polynucleotide of claim 1.

3. A host cell transformed with an expression vector of claim 2.

4. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP using the running parameters described above; and (c) sequences having at least 50% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

5. An isolated polynucleotide encoding a polypeptide of claim 4.

6.    An expression vector comprising an isolated polynucleotide of claim 5.

7.    A host cell transformed with an expression vector of claim 6.

5        8.    An isolated polypeptide comprising at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-
10   415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP using the running parameters described above; and (c) sequences having at least 50% identity to a sequence provided in SEQ ID NOS: 120-197, 275-348, 373-398, 406-409, 413-415, 417, 456-463 and 465, as measured by the computer algorithm BLASTP, using the running parameters and identity test defined above.

15

9.    A method for stimulating keratinocyte growth and motility in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

20   10.   The method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a)  SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398; (b) sequences having at least about 50% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 395, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

25

11.   A method for inhibiting the growth of cancer cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

30   12.   The method of claim 11, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of:  (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; and (b) sequences having at least 50% identity to a sequence of

SEQ ID NOS: 187, 196, 342, 343, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

13.     A method for modulating angiogenesis in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

14.     The method of claim 13, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a sequence of SEQ ID NOS: 187, 196, 342, 343, 397 and 398 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

15.     A method for inhibiting angiogenesis and vascularization of tumors in a patient, comprising administering to a patient a composition comprising a polypeptide of claim 4.

16.     The method of claim 15, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 342, 343, 397 and 398; and (2) sequences having at least 50% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

17.     A method for modulating skin inflammation in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

18.     The method of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 338 and 347; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 338 and 347 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

19.    A method for stimulating the growth of epithelial cells in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

20.    The method of claim 19, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of:  (a)  SEQ ID NOS: 129 and 348; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 129 and 348 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

21.    A method for inhibiting the binding of HIV-1 to leukocytes in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

22.    The method of claim 21, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of:  (a)  SEQ ID NOS: 340, 344, 345, 346 and 465; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

23.    A method for treating an inflammatory disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

24.    The method of claim 23, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of:  (a)  SEQ ID NOS: 340, 344, 345, 346 and 465; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm BLASTP using the running parameters and identity test defined above.

25.    A method for treating cancer in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.

26.    The method of claim 25, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 340, 344, 345, 346 and 465; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 340, 344, 345, 346 and 465 as measured by the computer algorithm

5   BLASTP using the running parameters and identity test defined above.


27.    A method for treating a neurological disease in a patient, comprising administering to the patient a composition comprising a polypeptide of claim 4.


10    28.    The method of claim 27, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of: (a) SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398; and (b) sequences having at least 50% identity to a sequence of SEQ ID NOS: 187, 196, 340, 342-346, 397 and 398, as measured by the computer algorithm BLASTP using the running parameters and identity test defined

15    above.

Figure 1

Distribution of human TAK1 mRNA in human tissues
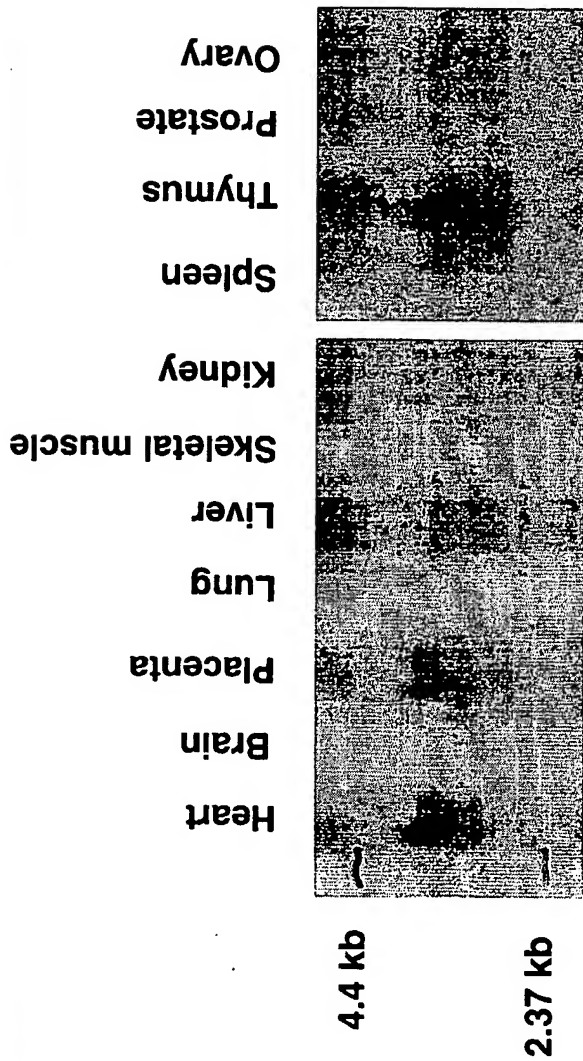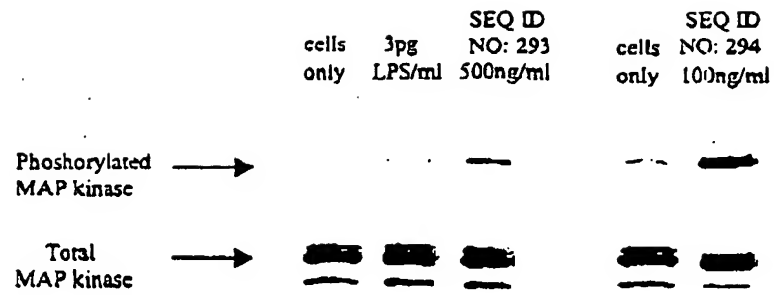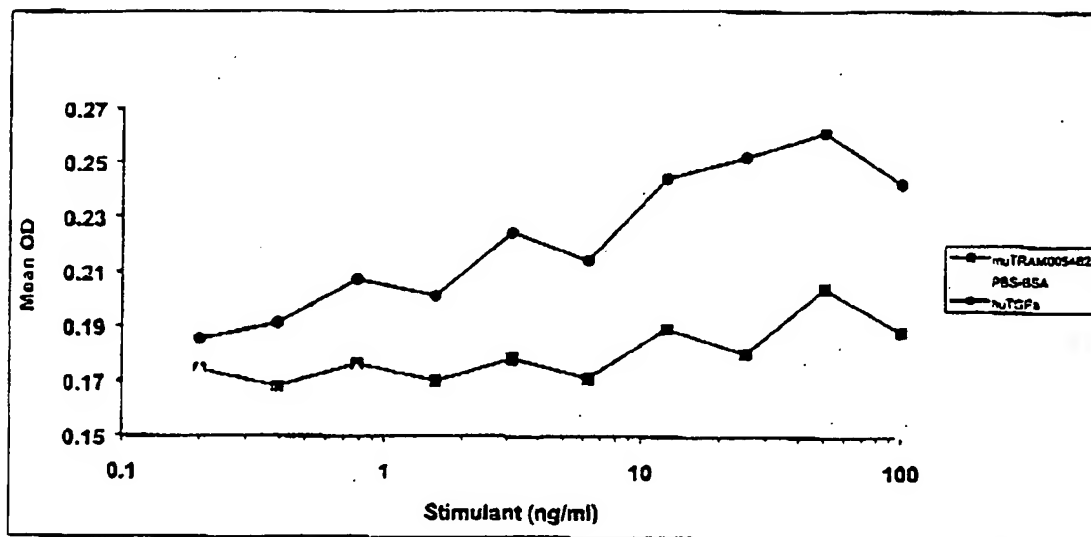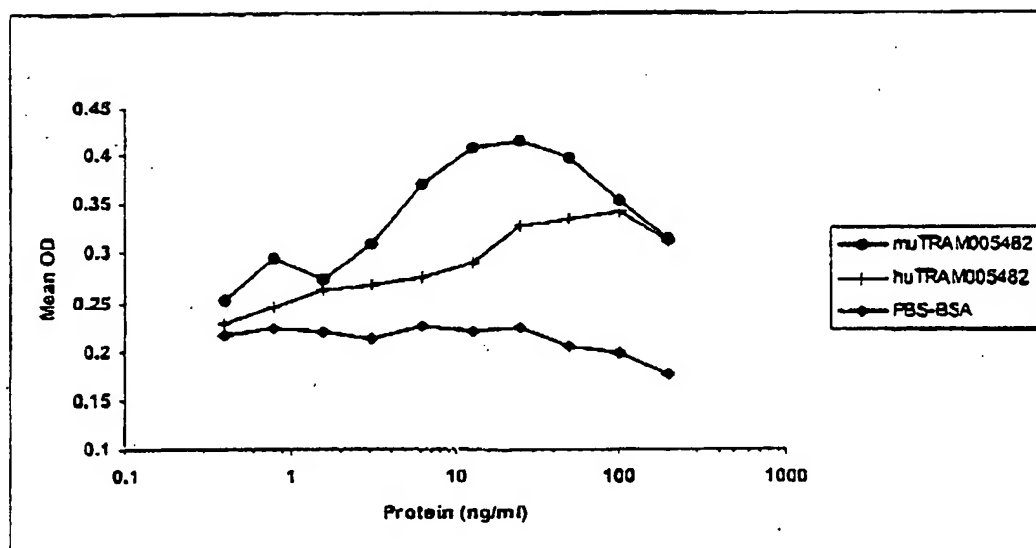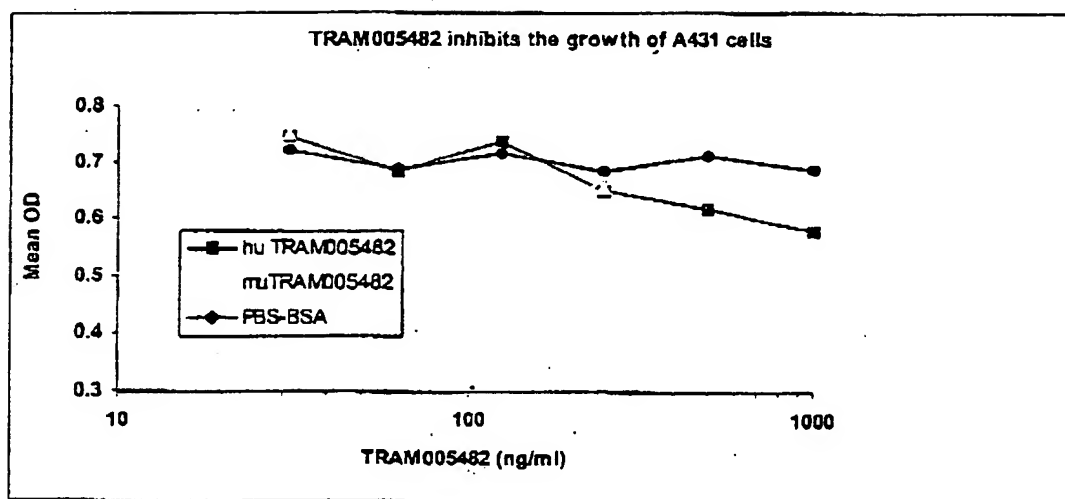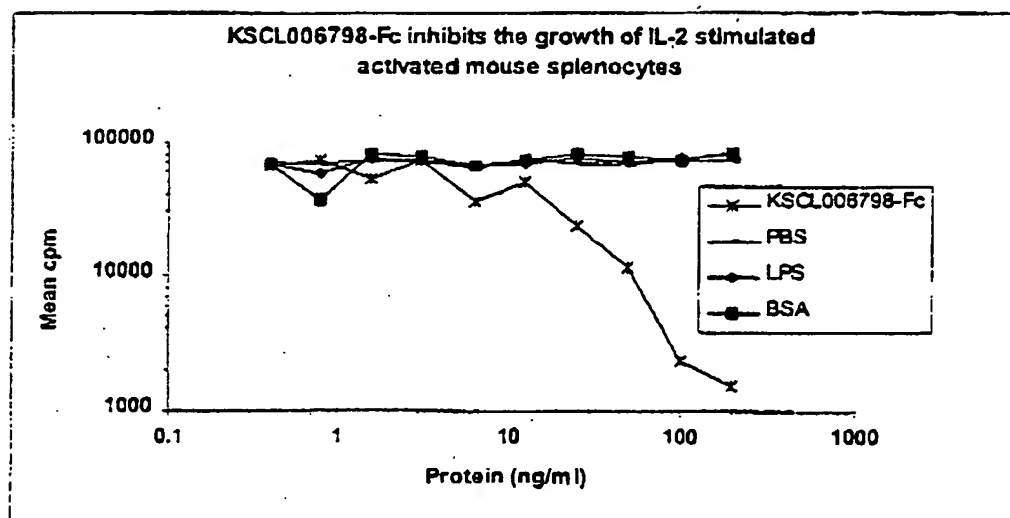
## Figure 2

Figure 3

## Figure 4

Figure 5



TRAM005482 inhibits the growth of A431 cells

**Figure 6**



KSCL006798-Fc inhibits the growth of IL-2 stimulated activated mouse splenocytes

Figure 7



KSCL007712 and apo-Transferrin act synergistically to induce the growth of IEC-18 cells

Figure 8



KS1 induces an oxidative burst in human peripheral blood mononuclear cells

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Figure 9



KS1 stimulates migration of THP-1 cells, a monocyte/macrophage cell line

Figure 10



IP injection of muKS1 induces a cellular infiltrate in C3/HeJ mice
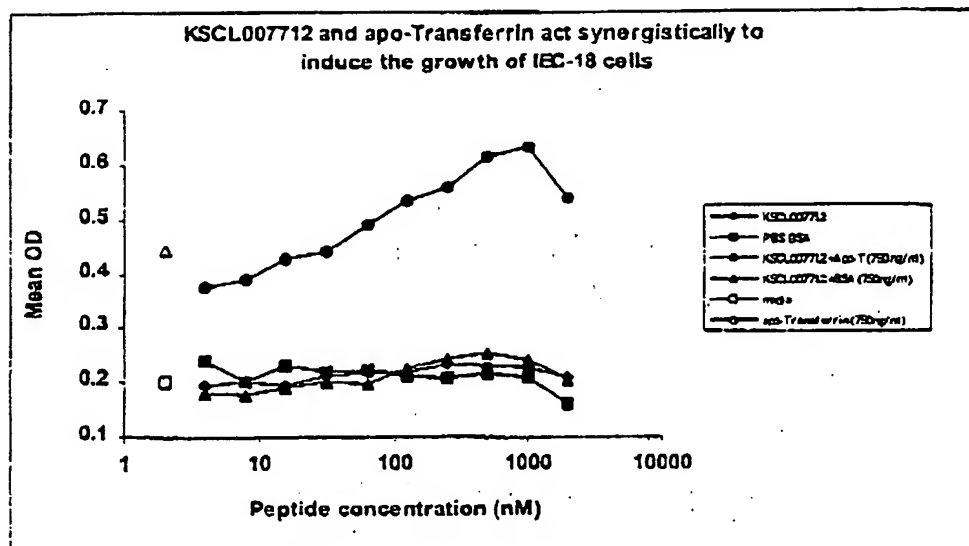
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Figure 11
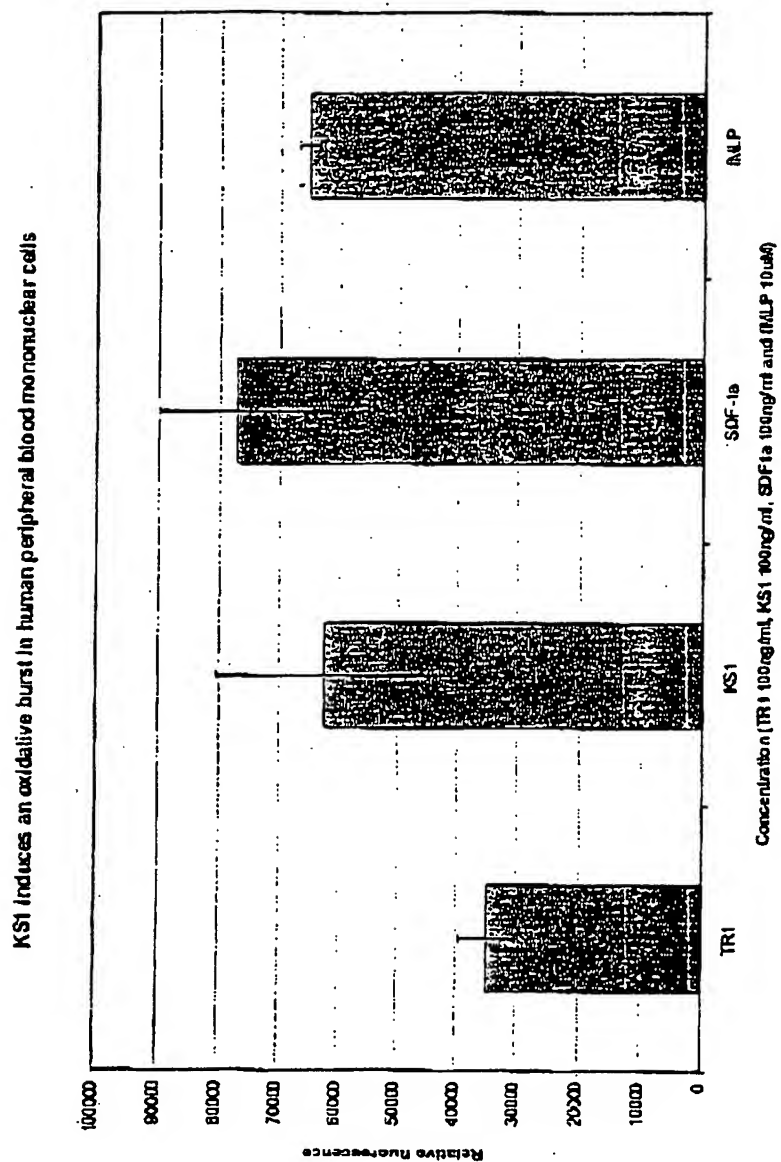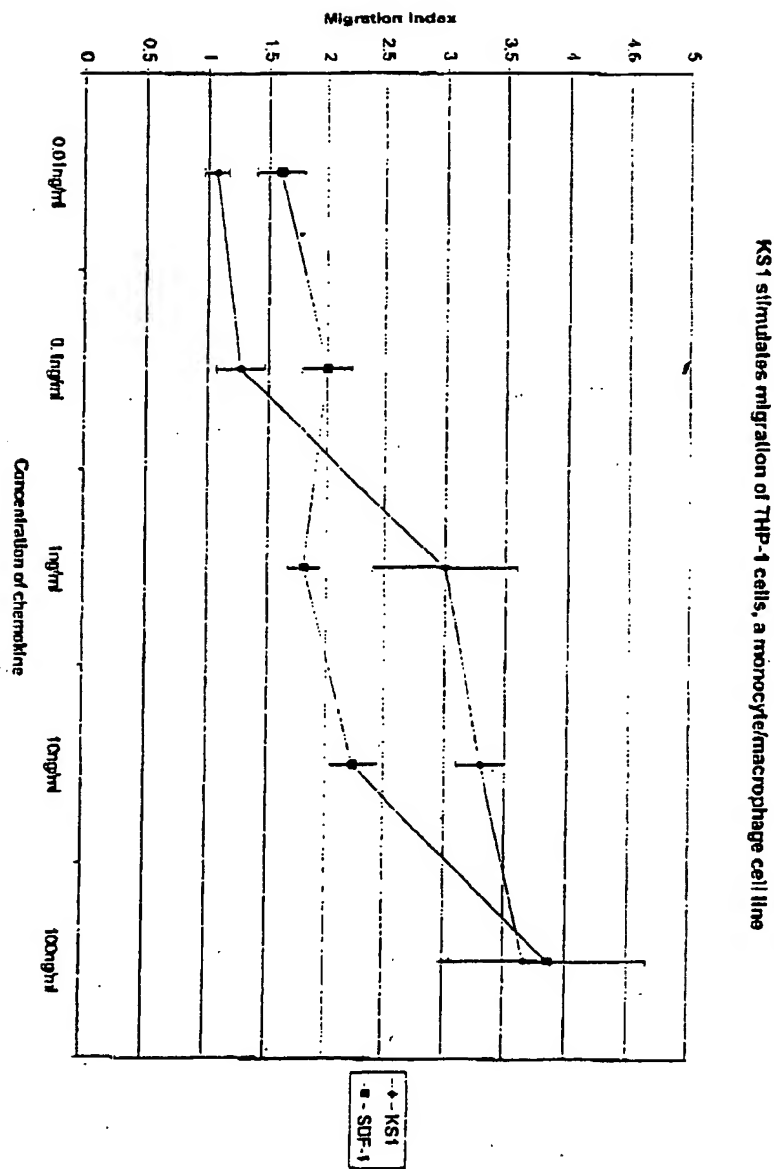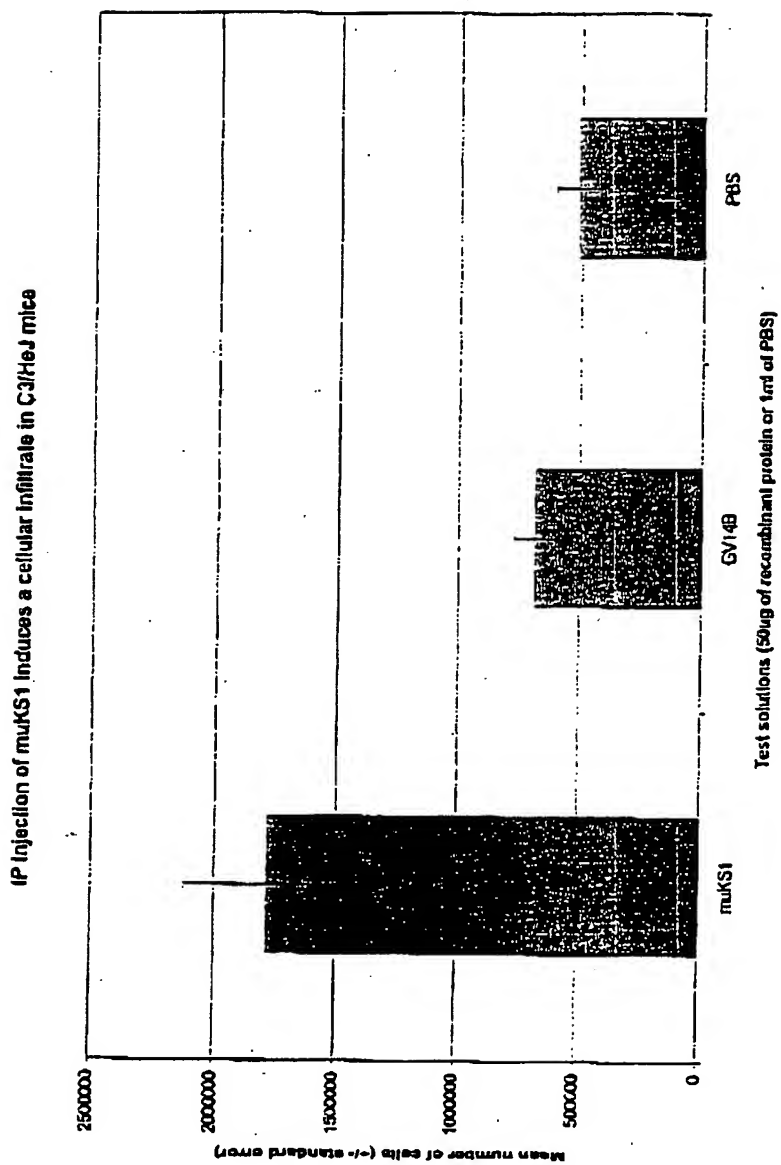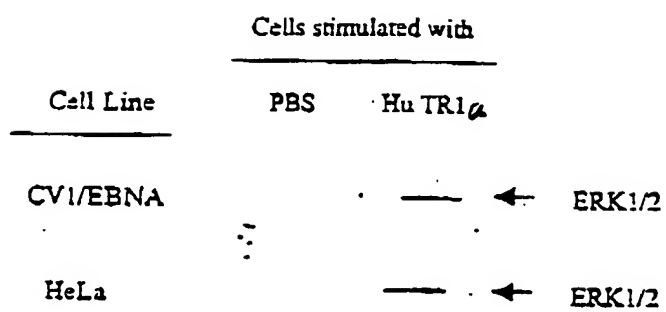
| Cell Line | Cells stimulated with | |
| --- | --- | --- |
| | PBS | Hu TR1α |
| CV1/EBNA | | ⎯ ← ERK1/2 |
| HeLa | | ⎯ ← ERK1/2 |

mu and huTR1 upregulate huTR1 mRNA expression in HeLa cells

HeLa cells stimulated with

PBS muTR1 huTR1 huTGFα
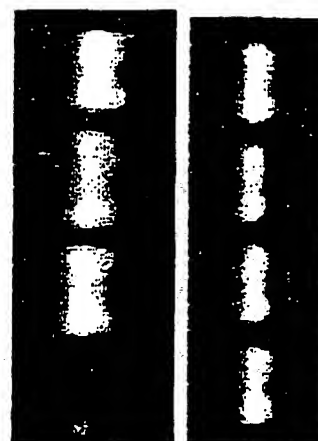
huTR1 mRNA

Actin mRNA

Figure 13A

Figure 13B



Murine Tr1 activates the SRE reporter in PC12SRE cells



Murine Tr1 activates the SRE reporter in HacatSRE cells
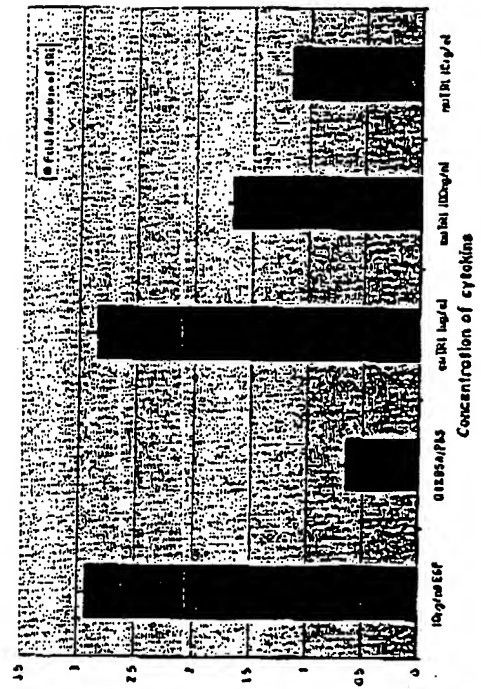
TR1 growth of HaCat cells is inhibited by an antibody to the EGF receptor
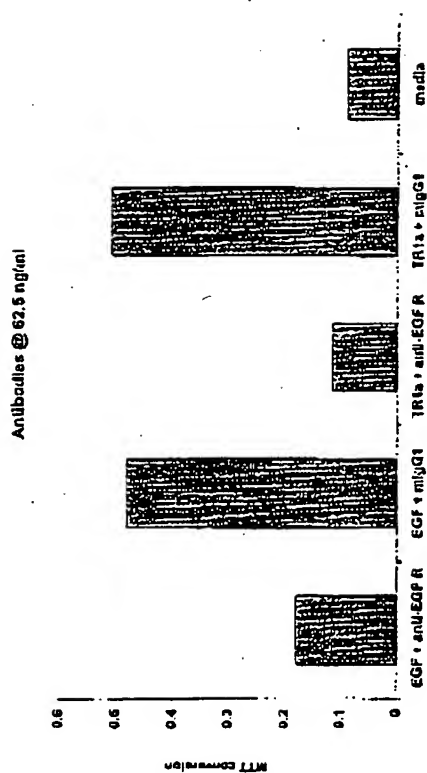
## Figure 15a

```
-202                                                                    GC
-200   AGCACCCAGC GCCAAGCGCA CCAGGCACCG CGACAGACGG CACGAGCACC
-150   CATCGACGGG CGTACTGGAG CGAGCCGAGC ACAGCAGAGA GAGGCGTGCT
-100   TGAAACCGAG AACCAAGCCG GGCGGCATCC CCCGGCCGCC GCACGCACAG
-50    GCCGGCGCCC TCCTTGCCTC CCTGCTCCCC ACCGCGCCCC TCCGGCCAGC


1      ATG AGG CTC CTG GCG GCC GCG CTG CTC CTG CTG CTC CTG GCG
1       M   R   L   L   A   A   A   L   L   L   L   L   L   A


43     CTG TGC GCC TCG CGC GTG GAC GGG TCC AAG TGT AAG TGT TCC
15      L   C   A   S   R   V   D   G   S   K   C   K   C   S


85     CGG AAG GGG CCC AAG ATC CGC TAC AGC GAC GTG AAG AAG CTG
29      R   K   G   P   K   I   R   Y   S   D   V   K   K   L


127    GAA ATG AAG CCA AAG TAC CCA CAC TGC GAG GAG AAG ATG GTT
43      E   M   K   P   K   Y   P   H   C   E   E   K   M   V


167    ATC GTC ACC ACC AAG AGC ATG TCC AGG TAC CGG GGC CAG GAG
57      I   V   T   T   K   S   M   S   R   Y   R   G   Q   E


211    CAC TGC CTG CAC CCT AAG CTG CAG AGC ACC AAA CGC TTC ATC
71      H   C   L   H   P   K   L   Q   S   T   K   R   F   I


253    AAG TGG TAC AAT GCC TGG AAC GAG AAG CGC AGG GTC TAC GAA
85      K   W   Y   N   A   W   N   E   K   R   R   V   Y   E


295    GAA TAG GGTGGACGAT CATGGAAAGA AAAACTCCAG GCCAGTTGAG AGA
98      E   ***


344  CTTCAGC AGAGGACTTT GCAGATTAAA ATAAAAGCCC TTTCTTTCTC ACA
394  AGCATAA GACAAATTAT ATATTGCTAT GAAGCTCTTC TTACCAGGGT CAG
444  TTTTTAC ATTTTATAGC TGTGTGTGAA AGGCTTCCAG ATGTGAGATC CAG
494  CTCGCCT GCGCACCAGA CTTCATTACA AGTGGCTTTT TGCTGGGCGG TTG
544  GCGGGGG GCGGGGGGAC CTCAAGCCTT TCCTTTTTAA AATAAGGGGT TTT
594  GTATTTG TCCATATGTC ACCACACATC TGAGCTTTAT AAGCGCCTGG GAG
644  GAACAGT GAGCATGGTT GAGACCGTTC ACAGCACTAC TGCTCCGCTC CAG
694  GCTTACA AAGCTTCCGC TCAGAGAGCC TGGCGGCTCT GTGCAGCTGC CAC
744  AGGCTCT CCTGGGCTTA TGACTGGTCA GAGTTTCAGT GTGACTCCAC TGT
794  GGCCCCT GTTGCAGGGC AATTGGGAGC AGGTCCTTCT ACATCTGTGC CTA
844  GAGGAAC TCAGTCTACT TACCAGAAGG AGCTTCATCC CCACCCCACC CCC
894  ACCCGCA CCCCAGCTCA TTCCCCTGTC ACGACCAGGC AAGTGATCCT TAA
944  AGGACCT GGGTCTTTTT CTTGCAAACT GAGGGTTTCT GAAAGGTCGG CTG
994  CTTTGGT AGAAGATGCT TCTGAGGCAT CCAAAGTCCC CAGCAGTGTG AGA
1044 AAATGAT TCTCGATGTT CGGGAGGACA AGGGAAGATG CAGGATTAGA TGC
1094 AGGACAC ACAGCCAGAG CTACACATCC TCTTGGCAAT GGGAGCTCCC CCC
1144 CCCCAAA GCTTTGTTTC TTTCCCTCAC CCCAACAGAA AGTGCACTCC CCC
1194 TCAGTGA ATACGCAAAC AGCACTGTTC TCTGAGTTAG GATGTTAGGA CGA
1244 TCCTGCG CCCTGCCCTC TCCTGTGTAC ATATTGCCTT CAGTACCCCT CCC
1294 CCACCCC ATGCCACACA CTGCCCCTCA TTAGAGGCCG CACTGTATGG CTG
1344 TGTATCT GCTATGTAAA TGCTGAGACC CCTGAGTGCT GCATGCAGGT TTC
1394 ATGTTCT TTCTAAGATG AAAAGAGAAA GTAATAAAAT ATATTTGAAG TTC
1444 CCCAAAA AAAAAAAAA A
```

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## Figure 15b

```
KLF-1      ..........  .........M  RLLAAA...L  LLLLLALCAS  RVDGS......  .K CKCSRKG
BRAK       ..........  .........M  RLPAAA...L  LLLLLALYTA  RVDGS......  ..KCKCSRKG
mCrg-2     ..........  ..........  MNPSAAVIFC  LILLGLSGTQ  GIPLAR....  TVRCNCIHID
mMig       ..........  ..........  MKSAVLFLLG  IIFLEQCGVR  GTLVIR....  NARCSCISTS
mSDF-1     ..........  ..........  MDAKVVAVLA  LVLAALCISD  GKPVSLS...  .YRCPCRFFE
mBLC       ..........  .........M  RLSTAT...L  LLLLASCLSP  GHGILEAHYT  NLKCRCSGVI
mMIP-2     .........M  AP.....PTC  RLLSAALVLL  LLLATNHQAT  GAVVAS....  ELRCQCLKTL
mKC        .........M  IP.....ATR  SLLCAA...L  LLLATSRLAT  GAPIAN....  ELRCQCLQTM
mLix       MSLQLRSSAH  IPSGSSSPFM  RMAPLA.FLL  LFTLPQHLAE  AAPSSVIAAT  ELRCVCLTVT

Consensus                                                                c c_
```

```
KLF-1      .PK.IRYSDVK  KLEMKPKYPH  CEEKMVIVTT  KSMSRYRGQE  HCLHPKLQST  KRFI....KW
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mLix       PK.INPKLIA   NLEVIPAGPQ  CPTVEVIAKL  K.....NQKE  VCLDPEAPVI  KKII....QK

Consensus                         C                       C
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KLF-1      YNAWNE.KRR  VYEE......  ..........
BRAK       YNAWNE.KRR  VYEE......  ..........
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mSDF-1     LNKRLKM...  ..........  ..........
mBLC       SLSSTPQAPV  SKRRAA....  ..........
mMIP-2     ILNKGK.AN.  ..........  ..........
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mLix       ILGSDK.KKA  KRNALAVERT  ASVQ......

Consensus
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1011c2PCTSEQUENCE LISTING

SEQUENCE LISTING

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    Watson, James D.
   Strachan, Lorna
   Sleeman, Matthew
   Onrust, Rene
   Murison, James G.
    Kumble, Krishanand D.

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     300
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          <213> Rat

1011c2PCTSEQUENCE LISTING
<220>


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gcggaagcag ccgcaggtat ggcggctgcc atgccgctgg gtttatcgtt gctgttgctg
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gaactcgtta tcactccgct gccttccggc gacgtggccg ccacattcca gttccgcacg
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        960
caggggaaga aagaggcctg tccattggca tctcagagcc tagtttatgt ggacatcaca
        1020
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        1057

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                <212> DNA
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        120
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        180
catgatctcc tggatgctct tggcctgtgc ccttccgtgt gctgctgacc caatgcttgg
        240

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1011c2PCTSEQUENCE LISTING
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gggttttcct ggtaaggatg gccaagacgg ccaggacgga gaccgagggg acagtggaga
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    660
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    720
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    750
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        <212> DNA
        <213> Rat

        <400> 20
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    240
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    300
gaagaaacca gaatttgata atgaaaagcc agctgctgtg gttgctcctc ttacaacagg
    360
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    420
cattacttta actggagttc atcaggttcc tgctgagaat gtgcaagtac acttcacaga
    480
gaggtcattt gatcttttgg taaaaaacct caatggcaag aattactcca tgattgtgaa
    540
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    660
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    720
attaatgaat gttctaaaga aaatttatga agatggagat gatgacatga agcgaaccat
    780
taataaagcg tgggtggaat cccgagagaa gcaagccagg gaagacacag aattcctgca
    840
gcccggggg
    849
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1011c2PCTSEQUENCE LISTING

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    120
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    180
gtagaggact cacagtcatg gggcttgcgc tctgccttgc ctctgcgggc atctctgggt
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    312

       <210> 22
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       <212> DNA
       <213> mouse

       <400> 22
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gagtcacccg aagcccctcc gcagtcctgg acacagctgt ggctcttccg cttcttgttg
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    240
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    480
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    600
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    780
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1011c2PCTSEQUENCE LISTING
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     1020
ggg 1023


     <210> 23
     <211> 997
     <212> DNA
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1011c2PCTSEQUENCE LISTING

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     240
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     360
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     420
gcatacagga gcaaagtaga taaaggatct gctgaggaag agaaaatcga tgtcatcctc
     480
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        <210> 25
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     660
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     780
cccctttgga gactggttcg agtatgtgtc ttctgctaac tacctagcag agctgatgat
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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING
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        600
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        660
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        720
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        778

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        <211> 1123
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        <213> Rat

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1011c2PCTSEQUENCE LISTING
1123

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   420
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      <213> Rat

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   180
tcctggcgtc tgggcctcct gggtcatcac catgaggcca cttcttgccc tgctgcttct
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1011c2PCTSEQUENCE LISTING
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        420
accgggacta cctgggccac gtggggagcc cgggccgcgt ggagaggcag gacctgtggg
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aaatggccaa tccatagctt ctttcttcca gtttttgggg gggtggccaa agccagcctc
        780
gctctcaggg ggtgcgatgg tgaggctaga acctgaggac caggtatggg ttcaggtggg
        840
tgtgggtgat tacattggca tctatgccag catcaaaaca gacagtacct tctctggatt
       ·900
tctcgtctat tctgactggc acagctcccc agtcttcgct taaaatacag tgaacccgga
        960
gctggcactt gctcctagtg gagggtgtga cattggtcca gcgcgcatac cagga
    1015
```

        <210> 31
        <211> 452
        <212> DNA
        <213> Human

        <400> 31
```
ttcgagcggc cgcccgggca ggttgaaact ttagaaagaa gagccgggag gatgtattgg
        60
ttgttaggaa aatgtaggct accagtagaa aatgacattc tctattaata agatctgagg
        120
tgcgacacac ataattgtcc caatttttaa gattgatggg gagcatgaag cattttttta
        180
atgtgttggc aggccccatt aaatgcataa actgcatagg actcatgtgg tctgaatgta
        240
ttttagggct ttctgggaat tgtcttgaca gagaacctca gctggacaaa gcagccttga
        300
tctgagtgag ctaactgaca caatgaaact gtcaggcatg tttctgctcc tctctctggc
        360
tcttttctgc tttttaacag gtgtcttcag tcaggagga caggttgact gtggtgagtc
        420
caggacacca aggcctactg cactcgggaa cc
    452
```

        <210> 32
        <211> 434
        <212> DNA
        <213> mouse

        <400> 32

1011c2PCTSEQUENCE LISTING

```
accaccaagc agatggaatg ctggcacacc catgcacctg catggcgtca caggtggaag
    60
attgttaaaa aattgacatc agaaatattt acagaaatag atacctgttt gaataaagtt
    120
agagatgaaa tttttgctaa acttcaaccg aagcttagat gcacattagg tgacatggaa
    180
agtcctgtgt ttgcacttcc tgtactgtta aagcttgaac cccatgttga aagcctcttt
    240
acatattctt tttcttggaa ttttgaatgt tcccattgtg dacaccagta ccaaaacagg
    300
tgtgtgaaga gtctggtcac ctttaccaat attgttcctg agtggcatcc actcaatgct
    360
gcccattttg gtccatgtaa cagctgcaac agtaaatcac aaataagaaa aatggtgttg
    420
gaaagagcgt cgcc
    434
```

```
    <210> 33
    <211> 903
    <212> DNA
    <213> mouse

    <400> 33
ctgcaacaag gctgttggtt cctctccaat gggctccagt gaagggctcc tgggcctggg
    60
ccctgggccc aatggtcaca gtcacctgct gaagacccca ctgggtggcc agaaacgcag
    120
ttttttcccac ctgctgccct cacctgagcc cagcccagag ggcagctacg tgggccagca
    180
ctcccagggc ctcggcggcc actacgcgga ctcctacctg aagcggaaga ggattttcta
    240
aggggtcgac accagagatg ctccaagggc ctgcaccaag ttgctttttgg gtttttttctg
    300
gtatttgtgt tttctgggat tttattttta ttatttttttt taatgtcctt tctttgggta
    360
atagagaaat ctctgcaaaa gactttgctg accaaccagc tggagctcaa ggaatgtggg
    420
gtatctgggg ccacaccatt acctgtgggc ttgctcctgg agccaaaccc tgcagcctta
    480
agagagaggg gcctgacctg ctctctttcc ctccctagct ccaggcctcc tctcctgcct
    540
cgtcactcct gtgttctggc ctcttgagtg cctttggagg tgtctctgac ctgtgaggat
    600
cagagacagt ccccgttttt aaacttcgac aattgacttt tatttccttt tctaattttt
    660
attatttttt aaaacaacca ggatgattat cacatctact cccccatccg tccagaaaag
    720
ccccaaattg attccttcag ggtctggcct gcccaggctc tattccacat gtgcaggttc
    780
caacagctta accctattct cttcccagtc atctgctgca ggtatagctg tctcatgccc
    840
ctgcctgcct attctggcca gtaccctaag ccccaagatc tccagcccct gccccagtat
    900
cct
    903
```

1011c2PCTSEQUENCE LISTING

&lt;210&gt; 34
&lt;211&gt; 1359
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;220&gt;
&lt;221&gt; unsure
&lt;222&gt; (644)...(644)

&lt;400&gt; 34

```
caaagaattc ggcacgagac cggcctcact atgtctgcca ttttcaattt tcagagtctg
60
ttgactgtaa tcttgctgct tatatgtaca tgtgcttata tccgatccct ggcacccagc
120
atcctggaca gaaataaaac tggactattg ggaatatttt ggaagtgtgc ccgaattggg
180
gaacgcaaga gtccttatgt cgccatatgc tgtatagtga tggccttcag catcctcttc
240
atacagtagc tttggaaact accagcatgt gcttgctatc agactgtaaa caaggacttg
300
cctccagaaa ataatgggaa gaatggttaa gccatttgtc tctgaacatg gaatgagata
360
aacttcaaga tgctgttctc tatttttatg ctattggacc aatgagctga atgaataatt
420
aagatgtaac agttcaatac acaggaatgt gattgtatcc atcaacctca gttctctcac
480
tccagtatta cattctgcaa atgtcattct gttgtgtcag gactgctttt cataaggttc
540
ttcgggcacg aagtagaaac ccagtggcaa attccaaggc tcctttgact agggcttcaa
600
aataatgtct tcacagaatg gtacctctag cgactgtcct attnttattg agaaaaaaac
660
ttgttctatt tttgttgttg ttactgttct tatggattgc attcatattt aaaccctttg
720
gattgctaac cagagtacct ctattcttgg caaattccgc agtttattac aggtgtttaa
780
agtattttaa acaaaactct gaatttcttt agttagccta agagttggct tctagtcaca
840
aagatacagc tgccacactg tgacgaagag caccttagaa agaaaagcag caagtgagcg
900
gtgagcaagt aagcaccgtg cagtcttcgt gcaagtaagc accgtgcagt cttcgttctc
960
tgtagtcttg tcttccaaat agaacgtcca tcgtagttac ccaaaggtgg tatttgtggt
1020
gttcttaatg cagtgcttta agtctagtgt atgttctgtc agcttgaact ggaatctctc
1080
ttgtaacttt gtaggttata aacatatctc atatctgctt tagtctgggt actatgctct
1140
aagtacattt cagctttgac acagaatgtg aatagacgaa tatcaaagga tacttacaag
1200
tttgtatcca acatttcttc aggttcagct gaaaatcagt tactgtttca aaacaaagag
1260
gaattaaatc ctagctgaaa actatacata gcatttatta attaattact gggtttaact
1320
```

1011c2PCTSEQUENCE LISTING
gctcttttta aaagtttgaa aaaaaaaaaa aaaaactcg
   1359

        <210> 35
        <211> 797
        <212> DNA
        <213> mouse

        <400> 35
aattcggcac gaggctagtc gaatgtccgg gctgcggacg ctgctggggc tggggctgct
    60
ggttgcgggc tcgcgcctgc cacgggtcat cagccagcag agtgtgtgtc gtgcaaggcc
    120
catctggtgg ggaacacagc gccggggctc ggagaccatg gcgggcgctg cggtgaagta
    180
cttaagtcag gaggaggctc aggccgtgga ccaagagctt tttaacgagt atcagttcag
    240
cgtggatcaa ctcatggagc tggccgggtt gagctgtgcc acggctattg ccaaggctta
    300
tcccccacg tctatgtcca agagtccccc gactgtcttg gtcatctgtg gccccggaaa
    360
taacggaggg gatgggctgg tctgtgcgcg acacctcaaa ctttttggtt accagccaac
    420
tatctattac cccaaaagac ctaacaagcc cctcttcact gggctagtga ctcagtgtca
    480
gaaaatggac attcctttcc ttggtgaaat gcccccagag gatgggatgt agagaaggga
    540
aaccctagcg gaatccaacc agacttactc atctcactga cggcacccaa gaagtctgca
    600
actcacttta ctggccgata tcattacctt gggggtcgct ttgtaccacc tgctctagag
    660
aagaagtacc agctgaacct gccatcttac cctgacacag agtgtgtcta ccgtctacag
    720
taagggaggt gggtaggcag gattctcaat aaagacttgg tactttctgt cttgaaaaaa
    780
aaaaaaaaaa aaactcg
    797

        <210> 36
        <211> 896
        <212> DNA
        <213> mouse

        <400> 36
ttaaggtttt cagactttat ttcatggtat ttgacattga cacatactga gttagtaaca
    60
agataccatg cagctccctc tagcctcgga tcaccgaagc aggaagaagg tcagactgcc
    120
cccatcccag atttgcttag tttgtctccc aatgtgctgg actttaaaga cagggaatgg
    180
agaagcagat ggatgcttca gtttcagtca tttttggctc tatagtgatc tctgccttcc
    240
tgtacctgtc cttggctgga ccctgggcag taactgtcac tcagatgagg acgatcatca
    300
ttacaatgga ccaactgagg gatgccctca tattagacca attaaaagtt gctgtgagtt

1011c2PCTSEQUENCE LISTING
```
     360
aaaccaggaa tgaccgcact tccacatcag aaatcaaaca aaatcaatgg ttgaagaaca
     420
tggttaggag cctggctagg tatctttgag agatggatgc agctggctac tcaggcaggt
     480
aagcaatgga ggtcagccac accctatcgt gatgcactcc ccatgttcag ggtaactgaa
     540
gaagtgggta aggccagctg aaggccagtc agggcaactt agatgtagcc tggcttctac
     600
ttccagcctc cggggacagg caaacacatt ttgggaagta agatgatgtc ccaattatta
     660
tcagtttttt gatatcacag tattgtcaca gggagcactg ggggtccagg ctagcctggg
     720
gtgaggctgg ccctcagcac acacaggaga gcagcttaag tgggacctaa aaaggaccca
     780
atgttacttg gtttaatgaa ggccccctca accccaacag cccctcctgc tcagggacac
     840
agttctcacc caattacaca ttaataacac acaaacagtg cctagcaatg ggccag
     896
```

```
     <210> 37
     <211> 501
     <212> DNA
     <213> mouse
```

```
     <400> 37
ctgcaggtcg acactagtgg atccaaagaa ttcggcacga gaatcatggc gccgtcgctg
     60
tggaaggggc ttgtaggtgt cgggcttttt gccctagccc acgctgcctt ttcagctgcg
     120
cagcatcgtt cttatatgcg actaacagaa aaggaagatg aatcattacc aatagatata
     180
gttcttcaga cacttctggc ctttgcagtt acctgttatg gcatagttca tatcgcaggg
     240
gagttcaaag acatggatgc cacttcagaa ttaaagaata agacatttga taccttaagg
     300
aatcacccat ctttttatgt gtttaaccat cgtggtcgag tgctgttccg gccttcagat
     360
gcaacaaatt cttcaaacct agatgcattg tcctctaata catcgttgaa gttacgaaag
     420
tttgactcac tgcgccgtta agctttttac aaattaaata acaggacaga cacagaattg
     480
agtattggag tttggggtgt a
     501
```

```
     <210> 38
     <211> 766
     <212> DNA
     <213> mouse
```

```
     <400> 38
gcagcaccca gcgccaagcg caccaggcac cgcgacagac ggcaggagca cccatcgacg
     60
ggcgtactgg agcgagccga gcagagcaga gagaggcgtg cttgaaaccg agaaccaagc
     120
```

1011c2PCTSEQUENCE LISTING

```
cgggcggcat ccccccggccg ccgcacgcac aggccggcgc cctccttgcc tccctgctcc
  180
ccaccgcgcc cctccggcca gcatgaggct cctggcggcc gcgctgctcc tgctgctcct
  240
ggcgctgtgc gcctcgcgcg tggacgggtc caagtgtaag tgttcccgga aggggcccaa
  300
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtacccac actgcgagga
  360
gaagatggtt atcgtcacca ccaaagagca tgtccaaggt accggggcca ggagcactgc
  420
ctgcacccta agctgcagag caccaaacgc ttcatcaagt ggtacaatgc ctggaacgag
  480
aagcgcaggg tctacgaaga ataggggtgga cgatcatgga aagaaaaact ccaggccagt
  540
tgagagactt cagcagagga ctttgcagat taaaataaaa gccctttctt tctcacaagc
  600
ataagacaaa ttatatattg ctatgaagct cttcttacca gggtcagttt ttacatttta
  660
tagctgtgtg tgaaaggctt ccagatgtga gatccagctc gcctgcgcac cagacttcat
  720
tacaagtggc tttttgctgg gcggttggcg ggggcgggg ggacct
  766
```

        <210> 39
        <211> 480
        <212> DNA
        <213> mouse

        <400> 39
```
ggcacgagga agcctcttcc catggaagca cactctagga gagagaaggc ctctgggctc
  60
cgcctggcct ggcattatga atgcagtggg gtcagtgtgt ggtggatgtg tgtactgggt
  120
tggctttcct ttttagtttt tttacttttt agtttagttt gttcttttcc ttccccaata
  180
aatcattctc acatgcttcc atgtttgttt ctgagaggtg ggggctcaaa tgtatagaaa
  240
gtaggcccca gtccataagg aggtgtgaac acacccctt actgcttatc acccatttga
  300
caggaacgcc caggagggga ggggagggg aagaggtgag ttctgcacag tcggacattt
  360
ctgttgcttt tgcatgttta atatagacgt tcctgtcgat ccttgggaga tcatggcctt
  420
cagatatgca cacgaccttt gaattgtgcc tactaattat agcaggggac ttgggtaccc
  480
```

        <210> 40
        <211> 962
        <212> DNA
        <213> mouse

        <400> 40
```
ggcacgagat tagcggctcc tcagcccagc aaatcctcca ctcatcatgc ttcctcctgc
  60
cattcatctc tctctcattc ccctgctctg catcctgatg agaaactgtt tggctttaa
```

1011c2PCTSEQUENCE LISTING

120
aaatgatgcc acagaaatcc tttattcaca tgtggttaaa cctgtcccgg cacaccccag
180
cagcaacagc accctgaatc aagccaggaa tggaggcagg catttcagta gcactggact
240
ggatcgaaac agtcgagttc aagtgggctg cagggaactg cggtccacca aatacatttc
300
ggacggccag tgcaccagca tcagccctct gaaggagctg gtgtgcgcgg gcgagtgctt
360
gcccctgccg gtgcttccca actggatcgg aggaggctac ggaacaaagt actggagccg
420
gaggagctct caggagtggc ggtgtgtcaa cgacaagacg cgcacccaga ggatccagct
480
gcagtgtcag gacggcagca cgcgcaccta caaaatcacc gtggtcacgg cgtgcaagtg
540
caagaggtac acccgtcagc acaacgagtc cagccacaac tttgaaagcg tgtcgccagc
600
caagcccgcc cagcaccaca gagagcggaa gagagccagc aaatccagca agcacagtct
660
gagctagacc tggactgact aggaagcatc tgctacccag atttgattgc ttggaagact
720
ctctctcgag cctgccattg ctctttcctc acttgaaagt atatgctttc tgctttgatc
780
aagcccagca ggctgtcctt ctctgggact agcttttcct ttgcaagtgt ctcaagatgt
840
aatgagtggt ttgcagtgaa agccaggcat cctgtagttt ccatcccctc ccccatccca
900
gtcatttctt taaaagcacc tgatgctgca ttctgttaca gtttaaaaaa aaaaaaaaaa
960
aa
962

          <210> 41
          <211> 794
          <212> DNA
          <213> mouse

          <400> 41
ggcacgaggc tagtcgaatg tccgggctgc ggacgctgct ggggctgggg ctgctggttg
60
cgggctcgcg cctgccacgg gtcatcagcc agcagagtgt gtgtcgtgca aggcccatct
120
ggtggggaac acagcgccgg ggctcggaga ccatggcggg cgctgcggtg aagtacttaa
180
gtcaggagga ggctcaggcc gtggaccaag agctttttaa cgagtatcag ttcagcgtgg
240
atcaactcat ggagctggcc gggttgagct gtgccacggc tattgccaag gcttatcccc
300
ccacgtctat gtccaagagt cccccgactg tcttggtcat ctgtggcccc ggaaataacg
360
gaggggatgg gctggtctgt gcgcgacacc tcaaactttt tggttaccag ccaactatct
420
attaccccaa aagacctaac aagcccctct tcactgggct agtgactcag tgtcagaaaa
480
tggacattcc tttccttggt gaaatgcccc cagaggatgg gatgtagaga agggaaaccc

1011c2PCTSEQUENCE LISTING
```
                                                           540
tagcggaatc caaccagact tactcatctc actgacggca cccaagaagt ctgcaactca
                                                           600
ctttactggc cgatatcatt accttggggg tcgctttgta ccacctgctc tagagaagaa
                                                           660
gtaccagctg aacctgccat cttaccctga cacagagtgt gtctaccgtc tacagtaagg
                                                           720
gaggtgggta ggcaggattc tcaataaaga cttggtactt tctgtcttga aaaaaaaaa
                                                           780
aaaaaaaact cgag
                                                           794


                   <210> 42
                   <211> 1152
                   <212> DNA
                   <213> mouse

                   <400> 42
ggcacgagct tctcagggcc tgccacccaa ataagtctgg ccctagcctc aactctctct
                   60
caggctgggc cacaggaagc tgctgactgg ccacttgaca ccctccccct aaagctaatg
                   120
tctgtgacta tagggaggtt agcacttttt ctaattggaa ttcttctctg tcctgtggcc
                   180
ccatccctca cccgctcttg gcctggacca gatacatgca gcctctttct ccagcacagc
                   240
ctttccctga gcctgaggtt agggcagagt ttagagggtg ggctaagtgt atgttttcat
                   300
gtatgcattc atgcctgtga gtgtgtggct tgctgtcgtg tcctctggga tcccaagcca
                   360
cgcgggtctt ccctctgtag atgggtcctg ggttctatca cctgcttatt tatgtacgag
                   420
gttgggggt ggacccaggg tgggttgatt gtctctttgt aaggaagtat gtgtcggggg
                   480
tgacacgagg ctaagcccga gaaaccccgg gagacagcac tgcataagaa actggtttcc
                   540
magactgcag agggagctgc acttttgttt tgaccaaaaa caaaaaacaa aacaaaacaa
                   600
aaacaaaaca aaataactc tgaagggcgg gaggataccc aagcctgatg cctgagagga
                   660
gtccctagac ttcagcaact ccgctgcgtg gcctgagccc agcgggaggg atggggagag
                   720
aatttttgg agtccgtgcc tgtggtgggc agtcctgagc cttcagctga agcagtgctt
                   780
tttggctgcc ctcacctcgc actacttgac cttgaggctc tgagtatctc ctgtgcacag
                   840
gagaagctcc tgcaccagaa agcaccaaar sccmtggcac cccatcttac tccactctcc
                   900
ccagggactc ccaggtggga actgctgtgg cagtgagctc agcccggaca gacactgcca
                   960
accctgtctc ctggcattgg gctccggctc tacctcccca agcagggcga ggccccgcct
                   1020
tctcagccta gcaccacctg tccccgagtc ttctcagctt gcccatcatt ctcggcgccc
                   1080
acacaggtga cagtcccaag tagataacct ccatgggaca agttgggtgt tgccttaccc
```

1011c2PCTSEQUENCE LISTING
1140
gcctgcccag cc
   1152

        <210> 43
        <211> 446
        <212> DNA
        <213> mouse

        <400> 43
ggcacgagct tgagtctgga gtgctgcaaa taatagtatg cactatccct gcctggcatg
   60
tttgtttgtt aatgtgcact ggtgtttttgc ctggatgtgt atacttgtga agatgtcaga
   120
actcctggag ctggagttag agacaatggt gagctgcctt gtggatgttg ggaattgaac
   180
ccaggtcctc tggagaaata accagtgctc ttaaccacta agccatctca acagccccaa
   240
attattttt taataagttg cctcggtcat gttgtcttaa tcagagcgat agaaaagtaa
   300
ctaatataga ttatttatga attcaggtgg cttaatggta tatgcatgaa ttagtagtaa
   360
aacaagaact agggccagca agtggcttaa gggtgcctgc taaccatctc agccacctga
   420
gttcagtctc caggaaccac acagtg
   446

        <210> 44
        <211> 391
        <212> DNA
        <213> mouse

        <400> 44
ggcacgagcc cacgtctatg ttcaccttcg ttgttctggt aatcaccatc gtcatctgtc
   60
tctgccacgt ctgctttgga cacttcaaat acctcagtgc ccacaactac aagattgaac
   120
acacagagac agatgccgtg agctccagaa gtaatggacg gcccccact gctggcgctg
   180
tccccaaatc tgcgaaatac atcgctcagg tgctgcagga ctcagagggg gacggggacg
   240
gagatggggc tcctgggagc tcaggcgatg agcccccatc gtcctcctcc caagacgagg
   300
agttgctgat gcctcctgat ggcctcacgg acacagactt ccagtcatgc gaggacagcc
   360
tcatagagaa tgagattcac cagtaagggg t
   391

        <210> 45
        <211> 516
        <212> DNA
        <213> Rat

        <400> 45
cctcctgtct ctgctgctac ttgtgaggcc tgcgcctgtg gtggcctact ctgtgtccct

1011c2PCTSEQUENCE LISTING

```
     60
cccggcctcc ttcctggagg aagtggcggg cagtggggaa gctgagggtt cttcagcctc
     120
ttccccaagc ctgctgccgc cccggactcc agccttcagt cccacaccag ggaggaccca
     180
gcccacagct ccggtcggcc ctgtgccacc caccaacctc ctggatggga tcgtggactt
     240
cttccgccag tatgtgatgc tcattgcggt ggtgggctcg ctgacctttc tcatcatgtt
     300
catagtctgc gcggcactca tcacgcgcca gaagcacaag gccacagcct actacccgtc
     360
ctctttcccc gaaaagaagt atgtggacca gagagaccgg gctggggggc cccatgcctt
     420
cagcgaggtc cctgacaggg cacctgacag ccggcaggaa gagggcctgg acttcttcca
     480
gcagctccag gctgacattc tggcttgcta ctcaga
     516
```

```
        <210> 46
        <211> 306
        <212> DNA
        <213> mouse


        <400> 46
gtcaccagca aaggtggaaa caaattcttt gaaggactct gacagccctg ggtctccaag
     60
gctgctggga ccagtcttag cctcttgtgg caagtggtag gaatgtgaat ctttgcgacc
     120
aggggggatca gaaatggggt ctcccatttc tggtgtctgc ccagtccttc caggtgggct
     180
cttcgtagcc ctggggtgga ttttcctcct cttccacaga gatgcttttt ctctgcatac
     240
catgtctgct ggtttcccaa aatctcccgc aaacccacac caccctccac tgaggctcag
     300
ccccag
     306
```

```
        <210> 47
        <211> 439
        <212> DNA
        <213> mouse


        <400> 47
gaaaactcgc aggacgctca ctggacagct gggctttttt tcagttgatt ttatggtttg
     60
catctttctc tttctctttt tctgtttctt gttccccttt cccctttttcc tggtgagaaa
     120
gcacatatta ctgagccatt gcaagcaatg ggaggggtcc acaatgacac acacacacac
     180
acacacacac atacacatac acacaccccc gagacagtgc cagagctaac agcctacatg
     240
tgtattttgg ccaaacttgg aaaataggtt ccttcttcg ttttgcttcc agccttttat
     300
ttgcaagtga tcttccatgc agtatgaaac atgcagacag cactggagtg tggcaagagt
     360
```

1011c2PCTSEQUENCE LISTING

gagcttgccc cacaagtctc tcggggatgt tgtactcttg tgtgtgttta cagtatcatg
    420
gctgttacat ctactggtc
    439


        <210> 48
        <211> 159
        <212> DNA
        <213> mouse

        <220>
        <221> unsure
        <222> (3)...(3)

        <400> 48
cangtacgct cactggaaca gcttgggctt ttttcagttg attttatggt ttgcatcttt
    60
ctctttctct ttttctgttt cttgttcccc tttcccttt tcctggtgag aaagcacata
    120
ttactgagcc attgcaagca atgggagggg tccacaatg
    159


        <210> 49
        <211> 465
        <212> DNA
        <213> Rat

        <400> 49
gtgccctccg ccgggtcggg atggagctgc ctgccgtgaa cttgaaggtt attctcctgg
    60
ttcactggct gttgacaacc tggggctgct tggcgttctc aggctcctat gcttggggca
    120
acttcactat cctggccctg ggtgctgtgg gctgtggccc agcgggactc tgttgatgcc
    180
attggcatgt ttcttggtgg cttggttgcc accatcttcc tggacattat ctacattagc
    240
atcttctact caagcgttgc cgttggggac actggccgct tcagtgccgg catggccatc
    300
ttcagcttgc tgctgcaagc ccttctcctg ctgcctcgtc taccacatgc accgggcagc
    360
gaggggtga gctcccgctc cgctcggatt tcttcggacc ttctcaggaa catagtgcct
    420
accagacaat tgactcgtca gactcacctg cagaccccct tgcaa
    465


        <210> 50
        <211> 337
        <212> DNA
        <213> Rat

        <220>


        <400> 50
ctcgtgccga aatcggcaga gcgtcgctcc tgtgctgtgg gnctaagctg gncgnctgtg

1011c2PCTSEQUENCE LISTING

60

gnatcgtcct cagcgnctgg ggagtgatca tgttgataat gctcgggata tttttcaatg

120

tccattctgc tgtggtaatt tagnatgtcc ccttcacaga gaaagatttt nagaacggcc

180

ctcagaacat atacaacctg tacgagcaag tcagctacaa ctgtttcatc gccgcgggcc

240

tctacctcct cctcgggggc ttctccttct gcnaagttcg tctcaataag cgcaaggaat

300

acatggtgcg ctagagcgna.gtccnactct ccccatt

337

<210> 51
<211> 371
<212> DNA
<213> Rat

<220>
<221> unsure
<222> (80)...(80)

<221> unsure
<222> (312)...(312)

<221> unsure
<222> (319)...(319)

<221> unsure
<222> (353)...(354)

<400> 51

gatgcgccct ggagccgact gggctgcggt ctgcgctttg tggccttcct ggcgaccgag

60

ctgctccctc ccttccagcn ggcgaattca gcccgacgag ctgtggcttt accggaaccc

120

gtacgtgaag gcggaatact tccccaccgg ccccatgttt gtcattgcct ttctcacccc

180

actgtccctg atcttcttcg ccaagtttct gaggaaagct gacgccgacc gacagcgagc

240

aagcctgcct cgctgccagc cttgccctag cgctaaatgg tgtctttacc aacatcataa

300

gactgatagt gngcaaggnc acgcccaaat tgcttctacc gagtgttccc cgnncgggat

360

tgcccattct t

371

<210> 52
<211> 228
<212> DNA
<213> Rat

<400> 52

ttccgcgggc gtcatgacgg ctgcggtgtt ctttggttgc gccttcatcg ccttcgggcc

60

cgcgctctcc ctttacgtct tcaccatcgc cactgatcct ttgcgagtca tcttcctcat

1011c2PCTSEQUENCE LISTING
```
      120
cgccggtgcc ttcttctggt tggtgtctct gctgctttcg tctgttttct ggttcctagt
      180
gagagtcatc actgacaaca gagatggacc agtacagaat tacctgct
      228
```

```
          <210> 53
          <211> 361
          <212> DNA
          <213> Human

          <400> 53
cgtggacact gctgaggaat gataccgagt ggtaggtcag aagaagatgc tgtgaacacc
      60
aggactttaa tcttatgctt gaaaatgcca gatgttgttc gggggacaac ttgtatcttt
      120
ctagcagcag atctgtagtt tgtatagcct caacaacaat tttaaataag atggagaata
      180
aattattgag gggactaggc tatatgcatt tgccttcatc cacccatgtt tattaagaat
      240
cattgtgctt aataatacca agactaagca ccataaccaa gaaatactaa tgtaaagatt
      300
gtttcttgtt tcaggaatgg ttaattcttc aacgttggta tgataatgat aacttgtttt
      360
g
      361
```

```
          <210> 54
          <211> 403
          <212> DNA
          <213> Human

          <220>

          <400> 54
ttgcgtggtc gcggccgagg tgtctgttcc caggagtcct tcggcggctg ttgtgtcagt
      60
ggcctgatcg cgatggggac aaaggcgcaa gtcgagagga aactgttgtg tctcttcata
      120
ttggcgatcc tgttgtgctc cctggcattg ggcagtgtta cagtgcactc ttctgaacct
      180
gaagtcagaa ttcctgagaa taatcctgtg aagttgtcct gtgcctactc gggctttct
      240
tctccccgtg tggagtggaa gtttgaccaa ggagacacca ccagactcgt ttgctataat
      300
aacaagatca cagcttccta tgaggaccgg gtgaccttct tgccaactgg tatcaccttc
      360
aagtccgtga cacgggaaga cactgggaca tacacttgta tgg
      403
```

```
          <210> 55
          <211> 413
          <212> DNA
          <213> Human
```

1011c2PCTSEQUENCE LISTING

<400> 55

```
tagcgtggtc gcggccgagg tacgactcgg tgctcgccct gtccgcggcc ttgcaggcca
    60
ctcgagccct aatggtggtc tccctggtgc tgggcttcct ggccatgttt gtggccacga
    120
tgggcatgaa gtgcacgcgc tgtggggggag acgacaaagt gaagaaggcc cgtatagcca
    180
tgggtggagg cataattttc atcgtggcag gtcttgccgc cttggtagct tgctcctggt
    240
atggccatca gattgtcaca gactttata acccttgat ccctaccaac attaagtatg
    300
agtttggccc tgccatcttt attggctggg cagggtctgc cctagtcatc ctgggaggtg
    360
cactgtctcc tgttcctgtc ctggggataa gagcagggct gggtacctgc ccg
    413
```

<210> 56
<211> 452
<212> DNA
<213> Human

<400> 56

```
ttcgagcggc cgcccgggca ggttgaaact ttagaaagaa gagccgggag gatgtattgg
    60
ttgttaggaa aatgtaggct accagtagaa aatgacattc tctattaata agatctgagg
    120
tgcgacacac ataattgtcc caatttttaa gattgatggg gagcatgaag cattttttta
    180
atgtgttggc aggccccatt aaatgcataa actgcatagg actcatgtgg tctgaatgta
    240
ttttagggct ttctgggaat tgtcttgaca gagaacctca gctggacaaa gcagccttga
    300
tctgagtgag ctaactgaca caatgaaact gtcaggcatg tttctgctcc tctctctggc
    360
tcttttctgc tttttaacag gtgtcttcag tcagggagga caggttgact gtggtgagtc
    420
caggacacca aggcctactg cactcgggaa cc
    452
```

<210> 57
<211> 190
<212> DNA
<213> Rat

<220>

<400> 57

```
ttcgcggccc ngtcgacggc attggcaaat agtcaaacct gggaagtaaa aagcaaaacc
    60
aaaaacaaaa ccaaagaaac aaactaaaac aaaacaagaa aaaccaacat ttcttcaatt
    120
cagtgtgcaa catatataaa acagaaatac taactctaca ggcagtatgt cgacgcggcc
    180
gcgtattcgg
    190
```

1011c2PCTSEQUENCE LISTING

&lt;210&gt; 58
&lt;211&gt; 413
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;400&gt; 58
ctgcaacaag gctgttggtt cctctccaat gggctccagt gaagggctcc tgggcctggg
      60
ccctgggccc aatggtcaca gtcacctgct gaagacccca ctgggtggcc agaaacgcag
      120
ttttttcccac ctgctgccct cacctgagcc cagcccagag ggcagctacg tgggccagca
      180
ctcccagggc ctcggcggcc actacgcgga ctcctacctg aagcggaaga ggattttcta
      240
aggggtcgac accagagatg ctccaagggc ctgcaccaag ttgctttttgg gttttttctg
      300
gtatttgtgt tttctgggat tttattttta ttattttttt taatgtcctt tctttgggta
      360
atagagaaat ctctgcaaaa gactttgctg accaaccagc tggagctcaa gga
      413

&lt;210&gt; 59
&lt;211&gt; 325
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;220&gt;
&lt;221&gt; unsure
&lt;222&gt; (213)...(213)

&lt;221&gt; unsure
&lt;222&gt; (223)...(223)

&lt;221&gt; unsure
&lt;222&gt; (227)...(227)

&lt;221&gt; unsure
&lt;222&gt; (243)...(243)

&lt;400&gt; 59
ggtatcaccc aggcccactt atccatctac agcgagtagt atggcggcct tccttgtaac
      60
aggcttttttc ttttctctct tcgtggtgct tgggatggaa cccagggctt tgtttaggcc
      120
tgacaaggct ctgcccctga gctgtgccaa gcccacctcc ctctgtgtac aaagctcctt
      180
tcttgggtga ccaacatctt cctgtctttg agnaaccagg ggncagnatg ggagccaccc
      240
agnagttaat taaaccaggt tcatcgggag tttgctgaaa tgttaagcat actctgttct
      300
agagagggag tgaagaaagg ggcca
      325

&lt;210&gt; 60

1011c2PCTSEQUENCE LISTING

&lt;211&gt; 372
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;400&gt; 60
ggccagcagg accgcggtca tgagcctctg caggtgtcaa caaggctcaa ggagcaggat
    60
ggatctcgat gtggttaaca tgtttgtgat tgcgggtggg accctggcca ttccaatcct
    120
ggcatttgtt gcgtctttcc tcctgtggcc ttcagcactg ataagaatct attattggta
    180
ctggcggagg acactgggca tgcaagttcg ctacgcacac catgaggact atcagttctg
    240
ttactccttc cggggcaggc caggacacaa gccatccatc cttatgctcc atggattctc
    300
cgcacacaaa ggacatgtgg ctcagcgtgg ccaagttcct tcccgaaaga acctgcactt
    360
tggctgtgtg ga
    372

&lt;210&gt; 61
&lt;211&gt; 363
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;220&gt;
&lt;221&gt; unsure
&lt;222&gt; (15)...(15)

&lt;400&gt; 61
gggcgcgcag gcggnaccgg tggcggcggg gctgctgctg gctaattggc acaggactgc
    60
gggccgcgac atggactgtc ctgtgcagcc cgaattccag cctcgttgta gccaggcaca
    120
ccaagagctt tccaccaaag aagcccctcc aagcactgac catgtctatt atggaccaca
    180
gccccaccac cggggtggta acggtcattg tcatcctcat cgccatagct gccctggggg
    240
gcttgatcct gggctgctgg tgctacctgc ggctgcagcg catcagccag tcagaggatg
    300
aggagagcat cgtgggtgat ggcgagacaa aggagccctt ttactggtgc agtactctgc
    360
taa
    363

&lt;210&gt; 62
&lt;211&gt; 399
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;400&gt; 62
aagggtcctg aagtcagttg ttgcatcaaa tacttcattt ttggcttcaa tgtcatattt
    60
tggtttttgg gaataacgtt tcttggaatc ggactgtggg cgtggaatga aaaaggtgtc
    120

1011c2PCTSEQUENCE LISTING

```
ctctccaaca tctcgtccat caccgacctc ggtggctttg acccagtgtg gcttttcctc
    180
tgagtggcca gcccgagcct gagctctgtc aatgacatcc aaggagaaaa tgaggttaat
    240
gagagacatt aattaaacac tccctcaccc caccgcacca aaccagttgg gttcttctga
    300
tattctggaa tactctgggc tatgttttat gtttatttct tttttaatcg gttgtatttt
    360
ggtctttttt tttcttcttc tttttctttt gctcccaaa
    399
```

        <210> 63
        <211> 399
        <212> DNA
        <213> mouse

        <220>

        <400> 63
```
caaagcccac tgtaggctcc gctgaggtag cgattgctgt atttctggtc atctgcatca
    60
tagtggtctt aaccatcctg ggctactgtt tcttcaagaa ccaaagaaag gaattccaca
    120
gtcccctgca ccacccacct cccacaccag ccagctccac tgtttccacc acagaggaca
    180
cagagcacct ggtctataat cacacaaccc agcctctctg agcctgggac tcttgccagt
    240
cttaccaggt cctgcttgcc aagacagaag ctagaacctg gaaaaacttg gggaccagac
    300
tcttcctacc tctttcctgg gcatacttac gctgtctcag aagacagatc tctgggcctc
    360
tcgcaggagt ctcagctgca ctcaggccag ttcctgggg
    399
```

        <210> 64
        <211> 2481
        <212> DNA
        <213> Rat

        <400> 64
```
gaactgtatc tggatgggaa ccagtttaca ctggtcccga aggaactctc caactacaaa
    60
catttaacac ttatagactt aagtaacaac agaataagca ccctttccaa ccaaagcttc
    120
agcaacatga cccaacttct caccttaatt ctcagttaca accgtctgag atgtatccct
    180
ccacggacct tgatggatt gaaatctctt cgtttactgt ctctacatgg aaatgacatt
    240
tctgtcgtgc ctgaaggtgc ctttggtgac ctttcagcct tgtcacactt agcaattgga
    300
gccaaccctc tttactgtga ttgtaacatg cagtggttat ccgactgggt gaagtcggaa
    360
tataaggaac ctggaattgc ccgctgtgcc ggtcccggag aaatggcaga taaattgtta
    420
ctcacaactc cctccaaaaa ttttacatgt caaggtcctg tggatgttac tattcaagcc
```

1011c2PCTSEQUENCE LISTING

```
     480
aagtgtaacc cctgcttgtc aaatccatgt aaaaatgatg gcacctgtaa caatgacccg
     540
gtggattttt atcgatgcac ctgcccatat ggtttcaagg gccaggactg tgatgtcccc
     600
attcatgcct gtacaagtaa tccatgtaaa catggaggaa cttgccattt aaaaccaagg
     660
agagaaacat ggatttggtg tacttgtgct gatgggtttg aaggagaaag ctgtgacatc
     720
aatattgatg attgcgaaga taatgattgt gaaaataatt ctacatgcgt tgatggaatt
     780
aacaactaca cgtgtctttg cccaccggaa tacacaggcg aactgtgtga ggaaaaactg
     840
gacttctgtg cacaagacct gaatccctgc cagcatgact ccaagtgcat cctgacgcca
     900
aagggattca agtgtgactg cactccggga tacattggtg agcactgtga catcgacttt
     960
gatgactgcc aagataacaa gtgcaaaaac ggtgctcatt gcacagatgc agtgaacgga
     1020
tacacatgtg tctgtcctga aggctacagt ggcttgttct gtgagttttc tccacccatg
     1080
gtcttccttc gcaccagccc ctgtgataat tttgattgtc agaatggagc ccagtgtatc
     1140
atcagggtga atgaaccaat atgccagtgt ttgcctggct acttgggaga gaagtgtgag
     1200
aaattggtca gtgtgtcaat tttggtaaac aaagagtcct atcttcagat tccttcagcc
     1260
aaggttcgac ctcagacaaa catcacactt cagattgcca cagatgaaga cagcggcatc
     1320
ctcttgtaca agggtgacaa ggaccacatt gctgtggaat ctatcgaggg cattcgagcc
     1380
agctatgaca ccggctctca cccggcttct gccatttaca gtgtggagac aatcaatgat
     1440
ggaaacttcc acattgtaga gctactgacc ctggattcga gtctttccct ctctgtggat
     1500
ggaggaagcc ctaaaatcat caccaatttg tcaaaacaat ctactctgaa tttcgactct
     1560
ccactttacg taggaggtat gcctgggaaa ataacgtgg cttcgctgcg ccaggcccct
     1620
gggcagaacg gcaccagctt ccatggctgt atccggaacc tttacattaa cagtgaactg
     1680
caggacttcc ggaaagtgcc tatgcaaacc ggaattctgc ctggctgtga accatgccac
     1740
aagaaagtgt gtgcccatgg cacatgccag cccagcagcc aatcaggctt cacctgtgaa
     1800
tgtgaggaag ggtggatggg gcccctctgt gaccagagaa ccaatgatcc ctgtctcgga
     1860
aacaaatgtg tacatgggac ctgcttgccc atcaacgcct tctcctacag ctgcaagtgc
     1920
ctggagggcc acggcggggt cctctgtgat gaagaagaag atctgtttaa ccccctgcca
     1980
ggtgatcaag tgcaagcacg ggaagtgcag gctctctggg ctcgggcagc cctattgtgg
     2040
atgcagcagt ggattcaccg gggacagctg acacagagaa tttcttgtcg aggggaacgg
     2100
```

1011c2PCTSEQUENCE LISTING

```
ataagggatt attaccaaag cagcagggta cgctgcctgt caaacgacta gaagtatctc
   2160
gcttggagtg cagaggcggg tgtgctgggg ggcagtgctg tggacctctg agaagcaaga
   2220
ggcggaaata ctctttcgaa tgcacagatg gatcttcatt tgtggacgag gtcgagaagg
   2280
tggtgaagtg cggctgcacg agatgtgcct cctaagtgca gctcgagaag cttctgtctt
   2340
tggcgaaggt tgtacacttc ttgaccatgt tggactaatt catgcttcat aatggaaata
   2400
tttgaaatat attgtaaaat acagaacaga cttatttta ttatgataat aaagaattgt
   2460
ctgcatttgg aaaaaaaaaa a
   2481
```

        <210> 65
        <211> 3008
        <212> DNA
        <213> mouse

        <220>
                <400> 65

```
tagacgggag cctgtggcta caagccactc agcctgatga cgccggccac tatacctgtg
   60
ttcccagcaa tggctttctg catccaccgt cagcttctgc ctatctcact gtgctctacc
   120
cagcccaggt gacagtcatg cctcccgaga cacccctgcc cactggcatg cgtggggtga
   180
tccggtgtcc ggttcgtgct aatcccccac tactgtttgt cacctggacc aaagacggac
   240
aggccttgca gctggacaag ttccctggct ggtccctggg cccagaaggt tccctcatca
   300
ttgcccttgg gaatgaggat gccttgggag aatactcctg caccccctac aacagtcttg
   360
gtactgctgg accctcccct gtgacccggg tgctgctcaa ggctcccccg gcttttatag
   420
accagcccaa ggaagaatat ttccaagaag tagggcggga gctactcatc ccgtgctccg
   480
cccggggaga ccctcctcct attgtctctt gggccaaggt gggccggggg ctgcagggcc
   540
aggcccaggt ggacagcaac aacagcctcg tccttcgacc cctgaccaag gaggcccagg
   600
gacgatggga atgcagtgcc agcaatgctg tagcccgtgt gaccacttcc accaatgtat
   660
atgtgctagg caccagcccc catgtcgtca ccaatgtgtc tgtggtacct ttacccaagg
   720
gtgccaatgt ctcttgggag cctggctttg atggtggcta tctgcagaga ttcagtgtct
   780
ggtatacccc actagccaag cgtcctgacc gagcccacca tgactgggta tctctggctg
   840
tgcctatcgg ggctacacac ctcctagtgc cagggctgca ggctcacgcg cagtatcagt
   900
tcagtgtcct tgctcagaat aagctgggca gtgggccctt cagtgagatt gtcctgtcta
   960
taccagaagg gcttcctacc acaccggctg cccctgggct gcctgcaacc aggagcagag
```

1011c2PCTSEQUENCE LISTING

1020
tgtgagcctg acttcccacg tggagagaag atcagaggcg gatcctggcg cagacgtttt
1080
cggtggcgtc gggcagccct gcgccgattc atcaggcagg cagctaggat gctcacaagg
1140
accgccacgc ccaagaagca gactccaccc acaacaccag ccaatacagg ctggggcagg
1200
agacctggta gctgtgtgcg ggaggggtac acctccaggc cggaagtgga gatgttggct
1260
acgttgctgg ggtcactgac gtagctatca gcgaaggcca cgaggcgaaa ctcatagaga
1320
acgtccttga tgaggccagg caccagcagc tggatttctg tgcccgccac accttggtcc
1380
aggatctccc agccttggga gccttgccgt ccctccagga tgtagccatc cagcctccca
1440
gggatgagtt ctgggggatc cctctgatct tctctccacg tgggaagtca ggctcacact
1500
ctgctcctgg ttcaggcagc cctgacagcg tgaccaagtt caagctccaa ggctccccag
1560
ttcccatcct acgccagagt ctgctctggg gggagcctgc tcgaccgcct agccctcacc
1620
cggattctcc acttggccgg ggacccttac cattagagcc catttgcagg ggcccagatg
1680
ggcgctttgt gatgggaccc actgtggccc cctcacaaga aaagttatgt ctggagcgcc
1740
cagaacctcg gacctcagct aaacgcttgg cccagtcctt tgactgtagc agtagcagcc
1800
ccagtggggt cccacaaccc ctctgcatta cagacatcag ccccgtgggg cagcctcttg
1860
cagccgtgcc tagccccta ccaggtccag gacccctgct ccagtatctg agcctaccct
1920
tcttccgaga gatgaatgtg gacggggact ggccacctct tgaggagccc acgcctgctt
1980
cggcttcaaa attcatggat agtcaagccc tgccccacct atctttcctt ccaccaccag
2040
actcacctcc tgcaaatctc agggcaagtg cttcctggga cactgatggg ggtcggggtc
2100
tcctcagagc ccccttacac agctttggct gattggactc tgagggagcg ggtcttgccg
2160
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2220
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2280
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2340
tgtggtgaca gtcacaaaaa ggaggaacca cctctgtgga tgagaactat gaatgggatt
2400
cggaattccc aggggacatg gagctgctag agacctggca cccaggcttg gccagttctc
2460
ggacccatcc tgaacttgag ccagagttag gtgtcaagac tccagaggag agctgtctcc
2520
tgaacccaac ccacgctgcc ggccccgagg cccgctgtgc tgcccttcgg gaggaattcc
2580
tagctttccg cagacgcagg gatgctacca gggcccggct accagcctat cagcagtcca
2640

1011c2PCTSEQUENCE LISTING
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tctcttaccc tgaacaggct actctgctat gagcccgctt agtgtgaaac taagaaaggc
   2700
ttatatggat ttgcaaagga gtccaagact ttggctccaa gctggggtac tgcccctacc
   2760
tctctgtgtc tcggtggcct ggtggtaggc ttgagtgagc ttggtataga gttggatgta
   2820
ctgactcttt aattgagttt gggagctgaa caggaatgtg tgtgtgtgtg tgtgtgtgtg
   2880
tgtgtgtgtg tgtgtgcgcg cgcaagcgca agcgcgagtt cgaaagtggt gtttatggtg
   2940
tgggtgcagg ttttttttt ttaaaaaaca ggtggataat aaatgtttgg aaccgttaaa
   3000
aaaaaaaa
   3008
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        <210> 66
        <211> 1888
        <212> DNA
        <213> mouse

        <220>
        <221> unsure
        <222> (1690)...(1690)

        <221> unsure
        <222> (1755)...(1755)

        <221> unsure
        <222> (1864)...(1864)

        <400> 66
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   120
cgccatgtgc actggaagac gtggctcgcg atcaagtgct cgcccagtct gcacgtcgac
   180
gacagggaac gaatggagct cctggaggaa gctaagaaga tggagatggc caagttccga
   240
tacattctac ctgtgtacgg catatgccag gaacctgtcg gcttggtcat ggagtacatg
   300
gagacaggct ccctggagaa gctgctggcc tcagagccat tgccttggga cctgcgcttt
   360
cgcatcgtgc acgagacagc cgtgggcatg aacttcctgc attgcatgtc tccgccactg
   420
ctgcacctag acctgaagcc agcgaacatc ttgctggatg cccactacca aatgtcaaga
   480
tttcttgact ttgggctggc caagtgcaat ggcatgtccc actctcatga cctcagcatg
   540
gatggcctgt ttggtacaat cggctacctc cctccagagc gaattcgtga aagagccgc
   600
ttgtttgaca ccaaacatga tgtatacagc ttcgccattg tgatctgggg tgtgcttaca
   660
cagaataatc catttgcaga tgaaaagaac atcctacaca tcatgatgaa agtggtaaag
   720
```

1011c2PCTSEQUENCE LISTING

```
ggccaccgcc cagagctgcc acccatctgc agaccccggc cgcgtgcctg tgccagcctg
    780
atagggctca tgcaacggtg ctggcatgca gacccacagg tgcggcccac cttccaagaa
    840
attacctctg aaacagaaga cctttgtgag aagcctgatg aggaggtgaa agacctggct
    900
catgagccag gcgagaaaag ctctctagag tccaagagtg aggccaggcc cgagtcctca
    960
cgcctcaagc gcgcctctgc tccccccttc gataacgact gcagtctctc cgagttgctg
   1020
tcacagttgg actctgggat cttcccaaga ctcttgaaag ccccgaaga gctcagccga
   1080
agttcctctg aatgcaagct cccatcgtcc agcagtggca agaggctctc gggggtgtcc
   1140
tcagtggact cagccttttc ctccagagga tcgctgtcac tgtcttttga gcgggaagct
   1200
tcaacaggcg acctgggccc cacagacatc cagaagaaga agctagtgga tgccatcata
   1260
tcaggggaca ccagcaggct gatgaagatc ctacagcccc aagatgtgga cttggttcta
   1320
gacagcagtg ccagcctgct gcacctggct gtggaggccg gacaggagga gtgtgtcaag
   1380
tggctgctgc ttaacaatgc caaccccaac ctgaccaaca ggaagggctc tacaccactg
   1440
catatggctg tggagcggaa gggacgtgga attgtggagc tactgctagc ccggaagacc
   1500
agtgtcaatg ccaaggatga agaccagtgg actgccctgc actttgcagc ccaaaatggg
   1560
gatgaaggcc agcacaaggc tgctgctaga gaagaatgct tctgtcaatg aggtggactt
   1620
tgagggccga acacccatgc atgtagcctg ccagcatgga caggagaaca ttgtgcgcac
   1680
cctgctccgn cgtggtgtgg atgtgggcct gcagggaaag gatgcctggt tgcctctgca
   1740
ctatgctgcc tgcanggcca ccttcccatt gttaagctgc tagccaagca gcctggggtg
   1800
agtgtgaatg cccagacact aacgggagga caccctgacc tgctgttcaa aggggcattt
   1860
accngtggct cgcattctca ttgacctg
   1888
```

<210> 67
<211> 1260
<212> DNA
<213> Rat

<400> 67
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gtgcgacaga ttcacaccag tgcaaccctba cccagatctg tatcaacacg gaaggagggt
120
acacctgctc ctgcactgat gggtactggc ttctggaagg gcagtgccta gatattgatg
180
aatgtcgcta tggttactgc cagcagctct gtgcgaatgt tcctggatcc tattcctgta
240
```

1011c2PCTSEQUENCE LISTING
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cgtgtaaccc tggcttcacc ctcaacgatg atggaaggtc ttgccaagat gtgaacgagt
     300
gtgaaactga gaacccctgt gttcagacct gcgtcaacac ctatggttct ttcatctgcc
     360
gctgtgaccc aggatatgaa ctggaggaag atggcattca ctgcagtgat atggatgagt
     420
gcagcttctc cgagttcctc tgtcaacatg agtgtgtgaa ccagccgggc tcatacttct
     480
gctcatgccc tccaggctac gtcttgttgg aagataaccg aagctgccag gatatcaatg
     540
aatgtgagca ccggaaccac acatgcactc ccctgcagac ttgctacaat ctgcaagggg
     600
gcttcaaatg tatcgacccc atcgtctgcg aggagcctta tctgctgatt ggggataacc
     660
gctgtatgtg ccctgctgag aatactggct gcagggacca gccattcacc atcttgtttc
     720
gggacatgga tgtggtatca ggacgctctg ttcctgctga catcttccag atgcaagcaa
     780
cgacccgata ccctggcgcc tattacattt tccagatcaa atctgggaac gagggtcgag
     840
agttctacat gcggcaaaca gggcctatca gtgccaccct ggtgatgaca cgccccatca
     900
aagggcctcg ggacatccag ctggacttgg agatgatcac cgtcaacact gtcatcaact
     960
tcagaggcag ctccgtgatc cgactgcgga tatacgtgtc ccagtatccg ttctgagcct
    1020
cgggttaagg cctctgacac tgcctttttac cacgccgagg gacaggagga gagaagaacc
    1080
ccaacgaggg acaggaggag agaagaaacc agcaagaatg agagcgagac agacattgca
    1140
cctttcctgc tgaacatctc cctggggcat cagcctagca tcctgacccc tacctgtact
    1200
atcgcaaact gtcactctga aggacaccat gccccagttc ctatgatgca gtagtatcca
    1260
```

        <210> 68
        <211> 1729
        <212> DNA
        <213> mouse

        <400> 68
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gaattcggca cgagcagaat atggctctgg gggttctgat agcagtctgc ctcttgttca
     60
aagcaatgaa ggcagcactg agcgaagaag cagaggtgat ccctcctagc acagcacagc
    120
agagcaactg gacatttaac aacaccgaag ctgactacat agaagaacct gtagctctga
    180
agttctctca tccttgtctg gaagaccata atagttactg cattaatgga gcatgtgcat
    240
tccaccatga gctgaagcaa gccatttgca gatgctttac tggttatacg ggacaacgat
    300
gtgagcattt gaccctaact tcgtatgctg tggattctta tgaaaaatac attgcgattg
    360
ggattggcgt cggattgcta attagtgctt ttcttgctgt cttctattgc tacataagaa
    420
```

1011c2PCTSEQUENCE LISTING

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aaaggtgtat aaatctgaaa tcaccctaca tcatctgctc tggagggagc ccattgtgag
      480
accttataag acatagtcat caagccattt gtcaaaagcc acagggaatc caatggagat
      540
ctttggatga tacaaaatgt gataagctaa cttgaaaata atggtggttt gggtcacaat
      600
gcagtaactg accattggtt cttagctttg gtcatcgttg ggtgccatgg aagctatggg
      660
aatgagctac agtaacagaa gccaagttca ctacccttct ttgggtttgc tgttgggtgg
      720
ttgttgtcac tgcaggaaga tttgttctat acttctgacc atctcagatg tgaattttca
      780
ttttaattgt tttctactac acatcaatca agtccaagta atgccatttc cgggttcttc
      840
gggcactcaa cattttgggc cacccgcctc gatggaccta atagcaaagt atctgtcctt
      900
atggaatttc agggaatttg gtatcaattt ttagatgaaa acagtgaatg tctcagctcc
      960
ttgagtgaac caaagatgca ttacacctaa accactaaaa gaaaatggaa tatccaaggc
     1020
agcataaatc ctacccagct ggtgacaaca gtttgcaaac ttcattcatg tagtttggaa
     1080
gaagcagata aattcctgag gactgaaagt cacctggaca gcagatccag agcaggcaaa
     1140
ggtagctggt tcctatatcg accataaagc ctgtgtgggc tcatctgtcc cctgatgttt
     1200
ttgcctatca tctcagcctt acattggaag actcacactt ggtatccatc gcttgaactg
     1260
aagttcgaca attcacctaa tgactaaaag cttacaattg ttcccaaaat atataggaac
     1320
aacagcatgt ggaatgtaac cattttttga cgtgttgata gcatatttgc acatgggtta
     1380
aaaaaagaaa cagtcgtaga aatacttatt agggaatcag tatccctcct tggaattgct
     1440
tctgctacat gattcaatct tgggcaagtc tcttatattc tttgtggttt ggttccattc
     1500
tctacaagac ccatgcagtt ccaaaattga actctaatag aactaaaaaa tacctcctat
     1560
aactgcatgg caggcaagat tatcctcaat gcttccatcc tcagccccgt ttctaaccct
     1620
caaataccca cgaatattat ccttactata tattgtcatg ttcagtttgt aaaataataa
     1680
cttattttga aaagaaataa aaaatgaaat tacaaagcaa aaaaaaaaa
     1729
```

```
         <210> 69
         <211> 355
         <212> DNA
         <213> Rat
```

```
<400> 69
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         60
  gccagctgca agttcattgt aaaagtacaa gtgagacgct gtcctattct gaaaccacca
        120
```

1011c2PCTSEQUENCE LISTING

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cagcatggct acctcacctg cagctcagcg ggggacaact atggtgcgat ctgtgaatac
      180
cactgcgatg gtggttatga acgccaaggg accccttccc gagtctgtca gtcaagtcga
      240
cagtggtctg gatcaccacc tgtctgtact cctatgaaga ttaatgtcaa tgttaactca
      300
gctgctggcc tcctggatca gttctatgag aaacagcgac tcctcatagt ctcag
      355
```

          <210> 70
          <211> 1421
          <212> DNA
          <213> Human

          <400> 70

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gattagcgtg gtcgcggccg aggtgtctgt tcccaggagt ccttcggcgg ctgttgtgtc
      60
agtggcctga tcgcgatggg gacaaaggcg caagtcgaga ggaaactgtt gtgtctcttc
      120
atattggcga tcctgttgtg ctccctggca ttgggcagtg ttacagtgca ctcttctgaa
      180
cctgaagtca gaattcctga gaataatcct gtgaagttgt cctgtgccta ctcgggcttt
      240
tcttctcccc gtgtggagtg gaagtttgac caaggagaca ccaccagact cgtttgctat
      300
aataacaaga tcacagcttc ctatgaggac cgggtgacct tcttgccaac tggtatcacc
      360
ttcaagtccg tgacacggga agacactggg acatacactt gtatggtctc tgaggaaggc
      420
ggcaacagct atggggaggt caaggtcaag ctcatcgtgc ttgtgcctcc atccaagcct
      480
acagttaaca tcccctcctc tgccaccatt gggaaccggg cagtgctgac atgctcagaa
      540
caagatggtt ccccaccttc tgaatacacc tggttcaaag atgggatagt gatgcctacg
      600
aatcccaaaa gcacccgtgc cttcagcaac tcttcctatg tcctgaatcc cacaacagga
      660
gagctggtct ttgatcccct gtcagcctct gatactggag aatacagctg tgaggcacgg
      720
aatgggtatg ggacacccat gacttcaaat gctgtgcgca tggaagctgt ggagcggaat
      780
gtggggggtca tcgtggcagc cgtccttgta accmtgattc tcctgggaat cttggttttt
      840
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      900
aagaaggtga tttacagcca gcctagtgcc cgaagtgaar gagaattcaa acagacctcg
      960
tcattcctgg tgtgagcctg gtcggctcac cgcctatcat ctgcatttgc cttactcagg
      1020
tgctaccgga ctctggcccc tgatgtctgk agtttmacag gatgccttat ttgtctttta
      1080
cacccacag ggcccctac ttcttcggat gtgtttttaa taatgtcagc tatgtgcccc
      1140
atcctccttc atgccctccc tccctttcct accactgmtg agtggcctgg aacttgttta
      1200
```

1011c2PCTSEQUENCE LISTING

aagtgtttat tccccatttc tttgagggat caggaaggaa tcctgggtat gccattgact
    1260
tcccttctaa gtagacagca aaaatggcgg gggtcgcagg aatmtacact caactgccca
    1320
cctggctggc aggatctttt gaataggtat cttgagcttg gttctgggct ctttccttgt
    1380
gtacctgccc gggcggccgc tcgaaatcaa gcttatcgat a
    1421

        <210> 71
        <211> 378
        <212> DNA
        <213> Human.

        <400> 71
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caggcgtaaa tgcaaaccgc ttccaactca aagcaagtaa cagcccacgg tgttctggcc
    120
aaagacatca gctaagaaag gaaactgggt cctacggctt ggactttcca accctgacag
    180
acccgcaaga caaaacaact ggttcttgcc agcctctaga gaaatcccag aacactcagc
    240
cctgacacgt taataccctg cacagatcag aggctgctgg ccacacagac tcaccaagcc
    300
acagacttgt cttccacaag cacgttctta ccttagccac gaagtgaccc aagccacacg
    360
tacctgcccg ggcggccg
    378

        <210> 72
        <211> 267
        <212> DNA
        <213> mouse

        <400> 72
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    60
agtgtagttg aggagcctgg ctgtggccct ggcaaggttc agaacggaag tggcaacaac
    120
actcgctgct gcagcctgta tgctccaggc aaggaggact gtccaaaaga aggtgcata
    180
tgtgtcacac ctgagtacca ctgtggagac cctcagtgca agatctgcaa gcactacccc
    240
tgccaaccag gccaaagggt ggaagtc
    267

        <210> 73
        <211> 1633
        <212> DNA
        <213> mouse

        <220>

        <400> 73

1011c2PCTSEQUENCE LISTING

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120
ggcatgtgac ccagtgtcgg ggacttgcat ctgtcctccc gggaagacgg gaggccattg
180
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240
gaatgggggc ctgtgtcatg ctaccaatgg cagctgctcc tgcccctgg gctggatggg
300
gccacactgt gagcacgcct gccctgctgg gcgctatggt gctgcctgcc tcctggagtg
360
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420
cttctatggt caagcttgtg aagacacctg ccctgccggc ttccatggat ctggttgcca
480
gagagtttgc gagtgtcaac agggcgctcc ctgtgaccct gtcagtggcc ggtgcctctg
540
ccctgctggc ttccgtggcc agttctgcga gaggggtgc aagccaggct tttttggaga
600
tggctgcctg cagcagtgta actgccccac gggtgtgccc tgtgatccca tcagcggcct
660
ctgcctttgc ccaccagggc gcgcaggaac cacatgtgac ctagattgca gaagaggccg
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780
cagtgggcag tgccactgtg tggacagcta cacgggaccc acttgccggg aagtgcccac
840
acagctgtcc tctatcagac cagcacccca gcactccagc agcaaggcca tgaagcacta
900
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1200
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1260
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gt    1560
acccctctgt aatgacatgc atgtaatgta atgcttcagt caccttaggg ttcttcctga
1620
cttccagctc tag

1011c2PCTSEQUENCE LISTING
1633

```
<210> 74
<211> 1252
<212> DNA
<213> mouse

<400> 74
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      120
ataccggatc agaattcagg ctatcaatga aattggagtt ggaccattta gtcagttcat
      180
taaagcaaaa actcggccat taccgccttc gcctcctagg cttgagtgtg ctgcgtctgg
      240
tcctcagagc ctgaagctca agtggggaga cagtaactcc aagacacatg ctgctggtga
      300
catggtgtac acactacagc tggaagacag gaacaagagg tttatctcaa tctaccgagg
      360
acccagccac acctacaagg tccagagact gacagagttt acctgctact ccttcaggat
      420
ccaggcaatg agcgaggcag gggaggggcc ttactcagaa acctacacct tcagcacaac
      480
caaaagcgtg cctcccaccc tcaaagcacc tcgagtgacg cagttagaag ggaattcctg
      540
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      600
ggtgctggtt ggaagagact ctgagtacaa gcaggtgtac aagggagaag aagccacatt
      660
ccaaatctca ggcctccaga gcaacacaga ttacaggttc cgcgtgtgtg cctgccgccg
      720
ctgtgtggac acgtctcagg agctcagtgg cgcgttcagc ccctctgcgg ctttcatgtt
      780
acaacagcgt gaggttatgc ttacagggga cctgggaggc atggaagaag ccaagatgaa
      840
gggcatgatg cccaccgacg aacagtttgc tgcactcatc gtgcttggct cgcgaccct
      900
gtccattttg tttgccttta tattacagta cttcttaatg aagtaaatcc agcaggccag
      960
tggtatgctc ggaacgccac acgttttaat acacatttac tcagagcctc cccttttac
     1020
gctgtttcgt tctttgattt atacgcttct cttgttttac acatttagct aggggaaaga
     1080
gtttggctgc acctatttga gatgcaaaac taggaagagg ttaaactgga tttttttta
     1140
aacaataata aataaaggaa taaagaagag aaggaagcgg cgggcaagct ccagacaccg
     1200
agagccagtg tgcccaacga gcttgccttg tcgggcttcc cgtgtgcttc tg
     1252

<210> 75
<211> 2411
<212> DNA
<213> mouse
```

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1011c2PCTSEQUENCE LISTING

&lt;400&gt; 75

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       120
agagtccttt ctacggcgac aagatgaact tgtattctct gtgtaagaag atagagcagt
       180
gtgactaccc gcctctcccg tcagatcact attcggagga gctacgacag ctagttaata
       240
tatgcatcaa cccagatcca gagaagcgac ccgacatcgc ctatgtttat gatgtggcaa
       300
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       360
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       420
gattactgtc tcagagctaa tgcgctttga atccttaacc agttttcata tgagcttcat
       480
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       540
agaatgcaag cccaacaaga gtttttcgtt tgagaattgt ttcgagtttc tgctgataga
       600
ctgtgtttat agatagtcag tgcccgatgg tgaagcacac acacataggc acatgtccag
       660
agcgatgcag aacctgagga aggacctggg catttgactt gtttgctttt aagtcactta
       720
atggacgttg tagtggacat gattgtgaac ttctgatttt tttcttttaa gtttcaagta
       780
catgttttag ttcttagcat tagagatctc aaatataatt cttataagac atgcagacat
       840
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       900
gtgaaagcat agaggtcaaa atgtgagttg gacactgaag tctatgtttt aatgcctttg
       960
aaagcctttt tttgtgtgtg tttaaatggt ataaatgaac ccattttaaa acgtggttaa
      1020
ggacttgttt gcctggcgtg atagtcatgt ttaacatgca caaggctttg tgtttttatt
      1080
gtacatttga agaatattct tggaataatc ttgcagtagt tatagttcaa tttctttaca
      1140
aatctaaata cacttaactc ataactatac actgtaatgc aagcatatat tgttattcat
      1200
atattgaagt tttgatcagt tcctcttcag aatctttttt atccaagtta ctttcttatt
      1260
tatattgtgt gtgcatttca tccattaaat gtttcagatt ttctgagaat gagttccctt
      1320
tttaaaatat atttggtatg ccaacacttt tttaggattg aaaaaaaatt tttttaaatg
      1380
tttgggtcat tctaggtgca tctgttttct cttgttagaa agaaaaggtg tgtgttaaaa
      1440
tgtgcctgtg aatgtcgata ttgtttggca gggttataat tttagagtat gctctagagt
      1500
atgttgaaca gcgtgaagac tggcccttac tgaagacaga actgttccaa gagcagcatt
      1560
cccgttgaga tgctttggag taaagtactg tgtatgacga tgacagacat tttagttaag
```

1011c2PCTSEQUENCE LISTING

```
      1620
ggggtgaaaa aaaaaggagg ggtatttagg aaaccctgag gtggaatttt ggtgaatgtc
      1680
ttcatcttaa taccagccaa ttccttcaga gaattgtgga gccaaagaac agagtaatcg
      1740
tggctgttgc agaacacggt gtgccatggt agagcattgg gaaggctcat cctgccggtg
      1800
ggtcggtcag acagccctgt gttggggagc ttgtactctg gcccacagag ctcggttgat
      1860
tttcttacag agtattcttt ctacagttat tttcaagtaa ttgtaaattt tcaaagtaat
      1920
atctcatctt ttaattcact atgtatgctg tcgtagacaa aggaaatctg ggtttttttt
      1980
tgtttttgtt tttgtttttt tttgtcttga aggctgaact gggtacatcc cagatcttag
      2040
tggctcatag gatatacccca gaggcatgaa gaaatggctt ccggtgacca tttgtgttgk
      2100
gktatatccc attgtaatgt cacaggactg attgagatga aacatcccct tcctacaaga
      2160
gttgtttct ttccatattt aaaaacatga ggttctgcct ggcagtgatg gtacacacct
      2220
ttaatcccag cacccgggag gcagaggcag gaggatttct gagttcgagg ccagcctggt
      2280
ctacaaagtg agttccagga cagccaggac tacacagaga aatcctgtct caaaaaacca
      2340
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      2400
caaaaaaaaa a
      2411
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        <210> 76
        <211> 1335
        <212> DNA
        <213> mouse

        <400> 76
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cctgtgcctg gctctgcact tatccccctc cctctctgcc agtgataatg ggtcctgcgt
      120
ggtccttgat aacatctaca cctccgacat cttggaaatc agcactatgg ctaacgtctc
      180
tggtgggggat gtaacctata cagtgacggt ccccgtgaac gattcagtca gtgccgtgat
      240
cctgaaagca gtgaaggagg acgacagccc agtgggcacc tggagtggaa catatgagaa
      300
gtgcaacgac agcagtgtct actataactt gacatcccaa agccagtcgg tcttccagac
      360
aaactggaca gttcctactt ccgaggatgt gactaaagtc aacctgcagg tcctcatcgt
      420
cgtcaatcgc acagcctcaa agtcatccgt gaaaatggaa caagtacaac cctcagcctc
      480
aaccctatt cctgagagtt ctgagaccag ccagaccata aacacgactc caactgtgaa
      540
cacagccaag actacagcca aggacacagc caacaccaca gccgtgacca cagccaatac
```

1011c2PCTSEQUENCE LISTING
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    600
cacagccaat accacagccg tgaccacagc caagaccaca gccaaaagcc tggccatccg
    660
cactctcggc agcccctgg caggtgccct ccatatcctg cttgtttttc tcattagtaa
    720
actcctctty taaagaaaac tggggaagca gatctccaac ctccaggtca tcctcccgag
    780
ctcatttcag gccagtgctt aaacataccc gaatgaaggt tttatgtcct cagtccgcag
    840
ctccaccacc ttggaccaca gacctgcaac actagtgcac ttgagggata caaatgcttg
    900
cctggatctt tcagggcaca aattccgctt cttgtaaata cttagtccat ccatcctgcg
    960
tgtaacctga agttctgact ctcagtttaa cctgttgaca gccaatctga acttgtgttt
    1020
cttgccaaag gtattcccat gagcctcctg ggtgtggggg tggggaggga atgatccttc
    1080
tttactttca aactgatttc agatttctgg ccaaacctac tcaggttgca aaggacttat
    1140
gtgacttatg tgactgtagg aaaaagagaa atgagtgatc atcctgtggc tactagcaga
    1200
tttccactgt gcccagacca gtcggtaggt tttgaaggaa gtatatgaaa actgtgcctc
    1260
agaagccaat gacaggacac atgacttttt ttttctaagt caaataaaca atatattgaa
    1320
caaggaaaaa aaaaa
    1335


        <210> 77
        <211> 440
        <212> DNA
        <213> mouse

        <220>

        <400> 77
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catcagctgc accggctcca ctcccatctg ctccaggccc tgaagagaag ccaacacttt
    120
tcaggcccct caacctccac atcagaacag gcagagcctg tggtgtcagc tgttgatcca
    180
aaggcaaccc ttggtggggt tggggttgta aagtagtgat gctaatttct aagcaacaag
    240
ctctgagctg cagcccccag gccctccagg gcagtccagg gcagtgccag ggttcagggt
    300
agttctaggg gtctagtatc tggatcaaca gtcccagag ttgggcccag tggctgctga
    360
cttgttcaat gaccaagaat atacgaccta accttttta tttggttggg caaccacagc
    420
tccgagtaag tcatcaaggc
    440


        <210> 78
        <211> 204
        <212> DNA
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1011c2PCTSEQUENCE LISTING

&lt;213&gt; mouse

&lt;400&gt; 78
ctccataaaa ttcctcaaaa tctgttcccc cagcagattt cctgtgccat cttgggctcc
        60
cttcctattc tttcccgtct ttagggcctc ctcacagtgt tgttttctaa caacgcaggc
        120
atgagaaggc actcactgtg tgctccctca ggcctggcct ctcctggtga ttgtcttctt
        180
cctctgtgtc ctcttcatcc caat
        204

&lt;210&gt; 79
&lt;211&gt; 300
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;220&gt;
&lt;

&lt;400&gt; 79
tatttatgac ttgggttaag ggagtttgct gtgcaatcat gaagaccaga gttcagatcc
        60
cagcacccat atagcaagag agcatacaag aagcacctgt gactgcactc tgaagaatcc
        120
aacaccttct tctggcctcc atggcacaca gaaccccca acacatgctc atccactctc
        180
aaagagacat acataaaaat aaatatttag gtcctgggtc cctcagagac tagtcttcac
        240
aggtcctaaa tacaaacga gcggaccgca aagggtgagg gagtggat gaagaagcta
    300

&lt;210&gt; 80
&lt;211&gt; 214
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;400&gt; 80
cccagaccct gtgtcagcta tcccagcaga aaaagaagat gcggaccctc tcagcaagtc
        60
aggtgaggaa acccaggaag cagggtcatg accccgcaga ggtcggggct cctggtgcag
        120
aggatcagat cttgtgtgac ttctgtcttg gggccagcag agtaagggca gtgaaatcct
        180
gtctgacctg catggtgaaa tactgtaagg agca
        214

&lt;210&gt; 81
&lt;211&gt; 152
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;220&gt;

1011c2PCTSEQUENCE LISTING
        <400> 81
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        60
cagtcatttt taagcacacg daccttttgt gagacagtcg tgatcttaac tgtggtgtca
        120
ctgatggagc tgaacggtat cccctaaaag ta
        152

        <210> 82
        <211> 181
        <212> DNA
        <213> mouse

        <220>


        <400> 82
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        60
gggtctccac ccacccacgc ccgctaaggt cacctgttct cccatggaga tgatgaagaa
        120
gctcatagct ggacaaggcc cggaacctca gcccagtaac cgacctactt cccgcctggg
        180
a
        181

        <210> 83
        <211> 332
        <212> DNA
        <213> mouse

        <220>


        <400> 83
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tttgttgttt ccctgtgtag ccctaacaag cctgtgtaga ccaggctggc tttaactttg
        120
cagatgacat tcacgtctac ttctctctgt gttggggtta tgggtctgca cacctgccca
        180
ggcctaggct gggggatttt gaagtatctt agattatgga gtagacccag agtttgcaag
        240
tatctgcttt aaagtgacac ataaacatag cctcctgacc atcttccaca gtgggaccct
        300
gatctggcct ctccctggaa gaagagagaa ag
        332

        <210> 84
        <211> 213
        <212> DNA
        <213> mouse

        <400> 84
gcaggcagat aacaatgatt actggacaga gtgcttcaac gcattggaac aggggaggca

1011c2PCTSEQUENCE LISTING

60
atatgtggat aatcccacag gcgggaaagt ggacgaggct ctggtgagaa gtgccaccgt
120
acattgttgg ccgcacagca acgtgctgga cacaagcatg ctctcatccc cagatgtggt
180
gcgcatgctg ctgtccctgc agcccttcct gca
213

      &lt;210&gt; 85
      &lt;211&gt; 273
      &lt;212&gt; DNA
      &lt;213&gt; mouse

      &lt;220&gt;


      &lt;400&gt; 85
ccggctctct ctctcctcct tccccgcctc ttctgcctcc cctgcctgga actctgatga
60
ggagggacca ggtggtcagg caccccagtc tgatcaggac tcctgtggcc tccagagttt
120
cactcccccg tccatcctga agcgggctcc tcgggagcgt ccaggtcacg tggcctttaa
180
cggcatcacc gtctactatt tcccacggtg ccagggattc accagtgtgc ccagccgtg
240
gtggctgtac cctgggcatg gcttctcggc aca
273

      &lt;210&gt; 86
      &lt;211&gt; 218
      &lt;212&gt; DNA
      &lt;213&gt; mouse

      &lt;400&gt; 86
ctcagccgcc tgctctgggg gctggagggt ctcccactta actgtgtctg ccgttcaggg
60
ggctcaccca gtgctgcgct acacagaggt tttccctcca gctccagtcc gtcctgccta
120
ctccttctat aaccgcctcc aagagctggc ctcactgttg ccccggccgg ataagccctg
180
cccagcctat gtggagccta tgactgtggt ttgtcacc
218

      &lt;210&gt; 87
      &lt;211&gt; 335
      &lt;212&gt; DNA
      &lt;213&gt; mouse

      &lt;400&gt; 87
gaggtggggt gggtgcatag cctgcctgca attgctgccg ctgggcttaa cgtgttgtga
60
gctggccggt ttcctacaca gcagcacctg ccatggagcc tggccacaag gccactcaga
120
gctgggtgga cagagtgtga ccagaaactc cctgtgggtt ctgataaagg attctcccat
180

1011c2PCTSEQUENCE LISTING

aggcaaggtt cagagaacct gggcctcctg ttctcaggga ggcctgtcta tccccagcct
    240
ctgagctgtt tcgtcctagt tggtgagtta agtggcatag ccctcttgag gcctctgatg
    300
tggaaggggc acagaattgc aattattctt gcatg
    335

        <210> 88
        <211> 410
        <212> DNA
        <213> mouse

        <400> 88
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gggaaactga aaagcaacct agggacactg taagcagaaa gctgaggctt ttaaaaaccc
    120
accttggcaa tgtaacttgg gaggttccca cacacccagg gctgtgcatc gtgaaattct
    180
gtctcctgag acgctgagaa acccttcctt gcagctataa tgggcctggc cgcccagtgt
    240
ggagctgtag cttcccacga cgtagccctc aggaacttca ggagggatgc cacagtctat
    300
ttctgaaaac aaaaccgtgt caacttcttt actttacaaa tgcaagtttt cagaatccac
    360
catctctctg cacccatacc ccatgcctca caccccagac cctgtgttag
    410

        <210> 89
        <211> 279
        <212> DNA
        <213> mouse

        <220>

        <400> 89
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    60
cacacacaca cacacacaca cacacacaca caccccaagg cttagagacc attgcagaag
    120
agaagagttt atgggaaatc ttggagaaaa cattggatgg tttgagagaa tggttaggag
    180
atcagactag ctagtccagg aagcagtgaa ggggggcggg gttagaagat gaggtcagaa
    240
gacagggtgg agggcattgt ccgacagaac cattgctgt
    279

        <210> 90
        <211> 398
        <212> DNA
        <213> mouse

        <400> 90
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1011c2PCTSEQUENCE LISTING

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        60
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       120
actcttagac atgggtgtgc tcactgaact ctagggtctg tgtgctagat gctgccaacg
       180
ctgtattcag gacctgaagt gagtaccgt gtggatccag accaatccag tgtgagacta
       240
ctgaagaaca tctgttgcca gaacggccac accaaacaga tggagtgccc cagcacttag
      ·300
cttcttaaat aacatcggaa ccattcagcc agcgagtctg tgtttgcttt ttgttaaatt
       360
gtccgccgaa tctaaattcc tccaaaaggc ttgtgacc
       398
```

        <210> 91
        <211> 279
        <212> DNA
        <213> mouse

        <400> 91
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        60
tggcgagaaa gcaagaccca gtggtagaca gattagcatt actgtacagc ttctttgggt
       120
gttcgaggaa gcccggctgg accatagtgg ccacggcggt gaggtaggcg tggacagggc
       180
tgaccagtcc aagttaagga cgttcgggtc catgttaacc ctgccttgta cgtccagcat
       240
cgtaagaaaa aacacttgag aacccgaaga ggagatgga
       279
```

        <210> 92
        <211> 401
        <212> DNA
        <213> mouse

        <400> 92
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        60
tgtagaatcg tattctttga aactgtactt agcagagcag aagaggcctg ctgacgctag
       120
cacgctctgc aatgaatcat gtggcaccga gtctacgcca aggcccccga gaaactttat
       180
tccatagatg ggcagatggt tcccaaagtt acactacaga actacaaatc gactcttaaa
       240
attaaaacgg gactttacaa gcattctaga agactcaaac ttgaagcaat ttttggaaaa
       300
taaatgtaca gagaaagat cttgaagcta ctgaacagag aaccctcatt aaccgagcaa
       360
atacatccta tggagcttcc gaggagtaca cagacagacc g
       401
```

        <210> 93
        <211> 339
        <212> DNA

1011c2PCTSEQUENCE LISTING
<213> mouse

<400> 93
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ccagcagtgc ctcggtaccc agaagacggg ctgtctcccc ccaaaagacg gcgacattcg
        120
atgagaagtc accacagtga tctcacattt tgcgagatta tcctgatgga gatggagtcc
        180
catgatgcag cctggccttt cctagagcct gtgaaccctc gcttggtgag tggataccga
        240
cgtgtcatca agaaccctat ggattttttcc accatgcgag aacgcctgct ccgtggaggg
        300
tacactagct cagaagagtt tgcagctgat gctctgctg
        339

        <210> 94
        <211> 55
        <212> DNA
        <213> mouse

        <400> 94
ggggtgtggg caacttggat aacctcagct gcttccatct ggctgacatc tttgg
        55

        <210> 95
        <211> 186
        <212> DNA
        <213> mouse

        <400> 95
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        60
gcggggcccc agaaacaaga agcgcggctg gaggaggctc gccgaggagc cgctggggtt
        120
agaggtcgac cagttcctgg aagacgtccg gctacaggag cgcacgaccg gtggcttgtt
        180
ggcaga
        186

        <210> 96
        <211> 244
        <212> DNA
        <213> mouse

        <400> 96
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        60
ccctctcccc aaggccatgg attatgaagc ccctctgtaa gatggtgagc caggggccct
        120
aagagggcat gaggcacacc ctgatcactg tctcaggcct ttgtgggcac tgactcgacc
        180
ctggcccacc tcacgccccc aggccagttg gcaactggtg gctcttgagg gctcttacgc
        240
cctt

1011c2PCTSEQUENCE LISTING

244

```
        <210> 97
        <211> 116
        <212> DNA
        <213> mouse

        <220>
        <221> unsure
        <222> (11)...(11)

        <221> unsure
        <222> (13)...(13)

        <221> unsure
        <222> (41)...(41)

        <400> 97
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    60
atctaggact cctgccaccc tgactgctga cttacagcta tgaggtcccg gcttct
    116

        <210> 98
        <211> 307
        <212> DNA
        <213> mouse

        <400> 98
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    60
cgaattcatg acacctgtga tccaggacaa cccctcaggc tggggtccct gtgccgttcc
    120
tgagcaattt cgggatatgc cctaccagcc attcagcaaa ggagatcggc tgggaaaggt
    180
tgcagactgg acaggggcca cataccagga caagaggtac acaaacaagt attcctctca
    240
gttcggtggg gggagtcagt atgcatattt ccatgaggag gatgagacaa gctttccagc
    300
tgggtgg
    307

        <210> 99
        <211> 360
        <212> DNA
        <213> mouse

        <220>

        <400> 99
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    60
tgtcccagca gaatccagtg acaggaagga gtttctgagg caggggagga ggcttctcca
    120
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1011c2PCTSEQUENCE LISTING
tgggaaccag acagccttgc ttcactgtat aagtgccctg atcacacgca gaatgaagtg
      180
ccaggttgct cagaagcaca aagggtgtgg ctactggccc taaccatgga ctacgtggtt
      240
ctaaccaaag actctagaac tctggggtgg gggagaaaca atgtgttctg tgctccagaa
      300
ctcggctt cctggcccat atggatgggc ttggcaagga acctacctct tctctaaggt
    360

        <210> 100
        <211> 257
        <212> DNA
        <213> mouse

        <400> 100
tgccgcgctg agaggggggg ccgcaccacc agcgccacca ccaccaccgc cgccgccgcc
    60
gggtggggtg ggaggggcgg gagccaccgc taccgccgcc gcctcccggg tgggcgccct
    120
tctccttaga cgccggcgac ccaggacgag ggcttcatca ctgtaaatgg ttgcaagccg
    180
acaaagctgc acctcctgaa aaagacggac agcccatcgc gtgagctgta gaaatttgtg
    240
gacgcatttc tatcggt
    257

        <210> 101
        <211> 203
        <212> DNA
        <213> mouse

        <400> 101
ccaaagtgcc cattgtgatt caagacgata gccttcccac ggggccccct ccacagatcc
      60
gcatcctcaa gaggcccacc agcaacggtg tggtcagcag ccccaactcc accagcaggc
      120
cagcccttcc tgtcaagtcc ctagcacagc gggaggcaga gtatgcagag gctcggagac
      180
ggatcctagg cagtgccagc cct
      203

        <210> 102
        <211> 300
        <212> DNA
        <213> mouse

        <400> 102
agtacagaga cctcggctgc agcttaaacc tcggacagtg caacgcccc tcaatcaagt
      60
agccaacccc aactcagcca tctttggggg agccaggccc agagaggaag tggttcagaa
      120
ggagcaagaa tgagcttagg ttgggaggga atggggcgtg ggggagctgg agcaagacca
      180
cggcctggtg gcagccggtc gccctacagg ccccattccc gcctggcact gtcctcctta
      240

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1011c2PCTSEQUENCE LISTING

cagcggaaac acagagcttg tgagtgcatg tcagctgtta acaagtggtt tctagtacat
300

```
<210> 103
<211> 370
<212> DNA
<213> mouse

<220>


<400> 103
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cagcaactgt ttcaggagct gcacggtgta cgcctgctga ctgatgcgct ggaactaaca
60

ctgggcgtgg cccccaaaga aaaccctccg gtgatgcttc agcccaaga gacggagagg
120

gccatggaga tcctcaaagt gctctttaat atcacctttg actctgtcaa gagggaagtt
180

gatgaggaag atgctgccct ttaccggtac ctggggactc ttctgcggca ctgcgtgatg
240

gttgaagctg ctggggaccg cacagaggag ttccacggcc acacggtgaa tctcctgggg
300

aacttgcccc tcaagtgttt ggatgtgctt ctggccctgg agctccacga aggatcctta
360

gagtcaatgg
370

```
<210> 104
<211> 423
<212> DNA
<213> mouse


<400> 104
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tttcccagcc tggtggagca gccgactggc gagtgtgcca actgtcccgt gcttcccagc
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tcctaccttg cctgtcttct ctctcctggg aagatgttcc tggtggggct gacgggaggc
120

atcgcctcag gcaagagctc cgtcatccag gtattccaac agctgggctg tgctgtaatc
180

gacgtggacg tcattgcgcg gcacgttgtc cagccagggt atcctgccca ccggcgtata
240

gtagaggcct ttggcactga agtcttgctg gagaatggcg acatcgaccg caaggtcctc
300

ggagacctga tcttcaacca gcctgaccgt cggcagctgc tcaactccat tacccaccct
360

gagatccgca aggaaatgat gaaggagacc ttcaagtact ctccgaggt accgatacgt
420

gat
423

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<210> 105
<211> 117
<212> DNA
<213> mouse
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1011c2PCTSEQUENCE LISTING
           <400> 105
agcttggtgc tgttcatatt taaactgata aagactcttc ataggagctg agggtagcaa
      60
gcccgcgtcg gtgactgggg tctcacacag gttcagcact tggagcatag tgaggtg
     117

           <210> 106
           <211> 133
           <212> DNA
           <213> mouse

           <400> 106
tttttttttt aaaataccac catttccaat cccaaaagaa catggcactt gtttgtttct
      60
tccccttctc attcattcca gactttcaag tgttttcttc aatactgagg ctttctcctg
     120
cagctctggt ctg
     133

           <210> 107
           <211> 217
           <212> DNA
           <213> mouse

           <220>
           <221> unsure
           <222> (1)...(1)

           <221> unsure
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           <221> unsure
           <222> (18)...(23)

           <221> unsure
           <222> (34)...(34)

           <221> unsure
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           <221> unsure
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           <221> unsure
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           <221> unsure
           <222> (55)...(58)

           <221> unsure
           <222> (152)...(152)

           <221> unsure
           <222> (155)...(155)

1011c2PCTSEQUENCE LISTING
           &lt;221&gt; unsure
           &lt;222&gt; (165)...(165)

           &lt;400&gt; 107
nttttttttg ngcgcacnnn nnngnnnncg cccnggnngn nnagcctacn nncannnngt
     60
tttcttctcc aggctgaaga cctgaacgtc aagttggaag gggagccttc catgcggaaa
     120
ccaaagcagc ggccgcggcc ggagcccctc ancanccca ccaangcggg cactttcatc
     180
gcccctcctg tctactccaa catcacccct taccaga
     217


           &lt;210&gt; 108
           &lt;211&gt; 346
           &lt;212&gt; DNA
           &lt;213&gt; mouse

           &lt;220&gt;

           &lt;400&gt; 108
gggcatagaa ggcatctcga aaagaatact tatttgaatt gaaggaagat gaagaggcct
     60
gcaggaaggc tcagaagaca ggagtgtttt acctctttca tgacctggat cctttgctcc
     120
aggcgtcagg acatcgatac ctggtgcccc ggcttagccg agcagagttg gaagggctgc
     180
tgggtaagtt cggacaggat tcgcaaagaa ttgaagattc ggtgctggtt gggtgctccg
     240
agcagcagga agcatggttt gctttggatc taggtctgaa gagtgcctcc tccagccgtg
     300
gacaagtatc gctgctccag cagcttgact gctgtaaaga ggatct
     346


           &lt;210&gt; 109
           &lt;211&gt; 242
           &lt;212&gt; DNA
           &lt;213&gt; mouse

           &lt;400&gt; 109
ccacattgtc cacaactgga aggcacgatg gttcatcctt cggcagaaca cgctcctgta
     60
ttacaagcta gagggtggcc ggcgagtaac cccgcccaag gggaggattg tccttgatgg
     120
ctgcaccatc acctgcccct gcctggagta tgaaaaccgg ccgctcctca ttaaactgaa
     180
gacccgaact tccactgagt acttcctgga agcctgttct cgagaggaga gagactcctg
     240
gg
     242


           &lt;210&gt; 110
           &lt;211&gt; 310
           &lt;212&gt; DNA
           &lt;213&gt; mouse

1011c2PCTSEQUENCE LISTING

&lt;220&gt;

&lt;400&gt; 110
cccggccggg ·aatccaggtg gtagctggtg gagtcgcctc cggagagtga cgcgcagact
    60
cggctccccc gcggcccgcc ctcctgccgg cctcgccgcg gtctcccttg ctccctgaga
    120
tcgctgagcg ctgagcagcg gcccgggaga ggaggccttg ggcgacgggg cgcggagagg
    180
gagggcgggc gggcagtggg ggcgccgcgg atctctatat ggcgacggct ctgtcgggtc
    240
tggctgtccg gctgtcgcgc tcggccgnc cgcccgctcc tatggggtct tctgcaa-gg
    300
ggctgacccg
    310

&lt;210&gt; 111
&lt;211&gt; 228
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;400&gt; 111
ttctttttta acatttggtg gttttttttct ttactctttt tttcttttcc ttctttttct
    60
gccctcaacc ccccaactcc tttggtatga agtacttttta acatttatat ttcattgtta
    120
cactttaaat tttgtaagga aaactctgat atttcattcc tcctgaacca ctaatgttag
    180
aatttatttc taagaatcag tcaacatgta tactcttaat agtgaatt
    228

&lt;210&gt; 112
&lt;211&gt; 292
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;400&gt; 112
gtggggtccc agacttgcca accaaagggc cattcctggt atatggttct ggcttcagct
    60
ctggtggcat ggactatggt atggttggtg gcaaggaggc tgggaccgag tctcgcttca
    120
aacagtggac ctcaatgatg gaagggctgc catctgtggc cacacaagaa gccaccatgc
    180
acaaaaacgg cgctatagtg gcccctggta agacccgagg aggttcacca tacaaccagt
    240
ttgatataat cccaggtgac acactgggtg gccatacggg tcctgctggt ga
    292

&lt;210&gt; 113
&lt;211&gt; 255
&lt;212&gt; DNA
&lt;213&gt; mouse

&lt;220&gt;

1011c2PCTSEQUENCE LISTING

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ttagatgact taggacttta atgttttcca tgcagtcgat tgaaaacact gatacatgaa
        60
caaccagaaa aagacctcag caatgtatag acctggaata tatagtgttg ccctggttaa
        120
actacaagaa cagccacgtg atcacagttt gagggtggaa ggcaggggtg tgactgagtt
        180
ttgtttaacg gcctaaccga aaagcaaaga atcaaccatt tcttctactt gtggcaagaa
        240
acgagagtca tggtg
        255

        <210> 114
        <211> 197
        <212> DNA
        <213> mouse

        <400> 114
gacccacatg tgaacagccg cgtgtatgtc acactgctct gtgtgtgatt tcttcacgtg
        60
tgcatgtgcg ctcttggtct ttccacttat tgcctcgttc gtaagaaacc aaccataagg
        120
tgccaaggag gttttattcc tttttttttt aaagatgaca aatgtacaga tgttagtaca
        180
gatgttaatg tacagat
        197

        <210> 115
        <211> 205
        <212> DNA
        <213> mouse

        <400> 115
aaaacatttc acaaaacagc aaaacaaaat tgatacaatc aaaaaaacaa cactataacc
        60
aacataggtg aaaacagcca aacacataat gtacaatctg gtgttccagg acaaacatct
        120
gtcatataca tggtatatac atatatactt tttcactcaa tatattatga caatatatat
        180
ttaaaatttt gttatagaca aaaaa
        205

        <210> 116
        <211> 202
        <212> DNA
        <213> mouse

        <220>

        <400> 116
cctccctcat cctctacttc ccttttcctt cctgcttgat tttctcattc cagaccccta
        60
tgcacacaca cacacacaca cacacacaca cacgaacaca cgcacacaca cacacacacg

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1011c2PCTSEQUENCE LISTING
                                                              120
cacacacaca ctgtccatcc atagttactt atttagtttt ccattcctag agagatctaa
     180
tcatcccta gtcagtgcct .aa
     202

          <210> 117
          <211> 240
          <212> DNA
          <213> mouse.

          <400> 117
ccgccaggag aggagataca cagccagtga tgtggaccac cggatggctg ttgctgctgc
     60
cgcttctgct gtgtgaagga gcgcaagccc tggagtgcta cagctgcgtg cagaaggcgg
     120
acgatggatg cgctccgcac aggatgaaga cagtcaaatg tggtcccggg gtggacgtct
     180
gtaccgaggc cgtgggagcg gtagagacca tccacgggca attctctgtg gcggtgcggg
     240

          <210> 118
          <211> 527
          <212> DNA
          <213> Human

          <400> 118
ccgtcagtct agaaggataa gagaaagaaa gttaagcaac tacaggaaat ggctttggga
     60
gttccaatat cagtctatct tttattcaac gcaatgacag cactgaccga agaggcagcc
     120
gtgactgtaa cacctccaat cacagcccag caaggtaact ggacagttaa caaaacagaa
     180
gctcacaaca tagaaggacc catagccttg aagttctcac acctttgcct ggaagatcat
     240
aacagttact gcatcaacgg tgcttgtgca ttccaccatg agctagagaa agccatctgc
     300
aggtgtttta ctggttatac tggagaaagg tgtgagcact tgactttaac ttcatatgct
     360
gtggattctt atgaaaaata cattgcaatt gggattggtg ttggattact attaagtggt
     420
tttcttgtta tttttactg ctatataaga aagaggtgtc taaaattgaa atcgccttac
     480
aatgtctgtt ctggagaaag acgaccactg tgaggccttt gtgaaga
     527

          <210> 119
          <211> 655
          <212> DNA
          <213> Rat

          <400> 119
atggcgcgcc ccgcgccctg gtggtggctg cggccgctgg cggcgctcgc cctggcgctg
     60
gcgctggtcc gggtgccctc agcccgggcc gggcagatgc cgcgccccgc agagcgcggg

1011c2PCTSEQUENCE LISTING

```
         120
ccccccagtac ggctcttcac cgaggaggag ctggcccgct acagcggcga ggaggaggat
         180
caacccatct acttggcagt gaagggagtg gtgttcgatg tcacctctgg gaaggagttt
         240
tatggacgtg gagcccccta caacgccttg gccgggaagg actcgagcag aggtgtggcc
         300
aagatgtcgc tggatcctgc agacctcact catgacattt ctggtctcac tgccaaggag
         360
ctggaagccc tcgatgacat cttcagcaag gtgtacaaag ccaaataccc cattgttggc
         420
tacacggccc gcaggatcct caacgaggat ggcagcccca acctggactt caagcctgaa
         480
gaccagcccc attttgacat aaaggacgag ttctaatgtc tagctgagaa gctggttcta
         540
gggagaggtg aggggacagg agttaaatgt cccacggaac aagcagggga agcctctgag
         600
tgctctgcat ctgaataaaa ctgatattta actgggaaaa aaaaaaaaaa aaaaa
         655
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```
        <210> 120
        <211> 176
        <212> PRT
        <213> Rat

        <400> 120
Met Val Pro Cys Phe Leu Leu Ser Leu Leu Leu Val Arg Pro Ala
 1               5                  10                  15
Pro Val Val Ala Tyr Ser Val Ser Leu Pro Ala Ser Phe Leu Glu Glu
            20                  25                  30
Val Ala Gly Ser Gly Glu Ala Glu Gly Ser Ser Ala Ser Ser Pro Ser
            35                  40                  45
Leu Leu Pro Pro Arg Thr Pro Ala Phe Ser Pro Thr Pro Gly Arg Thr
    50                  55                  60
Gln Pro Thr Ala Pro Val Gly Pro Val Pro Pro Thr Asn Leu Leu Asp
65                  70                  75                  80
Gly Ile Val Asp Phe Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val
                    85                  90                  95
Gly Ser Leu Thr Phe Leu Ile Met Phe Ile Val Cys Ala Ala Leu Ile
                100                 105                 110
Thr Arg Gln Lys His Lys Ala Thr Ala Tyr Tyr Pro Ser Ser Phe Pro
            115                 120                 125
Glu Lys Lys Tyr Val Asp Gln Arg Asp Arg Ala Gly Gly Pro His Ala
            130                 135                 140
Phe Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Gln Glu Glu Gly
145                 150                 155                 160
Leu Asp Phe Phe Gln Gln Leu Gln Ala Asp Ile Leu Ala Cys Tyr Ser
                    165                 170                 175

        <210> 121
        <211> 116
        <212> PRT
        <213> Rat

        <400> 121
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1011c2PCTSEQUENCE LISTING

```
Met Glu Leu Leu Tyr Trp Cys Leu Leu Cys Leu Leu Leu Pro Leu Thr
1               5                   10              15
Ser Arg Thr Gln Lys Leu Pro Thr Arg Asp Glu Glu Leu Phe Gln Met
            20                  25              30
Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
        35                  40              45
Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
    50                  55              60
Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
65                  70              75                  80
Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
            85                  90              95
Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
            100                 105             110
Gln Lys Gln Gln
            115
```

```
        <210> 122
        <211> 64
        <212> PRT
        <213> Human

        <400> 122
Met Asn Leu Leu Ile Gly Ser Ile Ile Leu Ser Ser Phe Leu Val Leu
1               5                   10              15
Ser Asp Gly Asp Thr Thr Ala Ser Pro Ser Ser Met Ser Ser Ser Ser
            20                  25              30
Val Leu Asn His Ile Ser Ser Ser Ser Ser Val Trp His Leu Phe
        35                  40              45
Asp Ile Cys Asp Ser Ser Lys Trp Asn Ala Tyr Cys Gln Val Trp Gly
    50                  55                  60
```

```
        <210> 123
        <211> 68
        <212> PRT
        <213> Human

        <400> 123
Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg
1               5                   10              15
Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly
            20                  25              30
Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr
        35                  40              45
Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe
    50                  55                  60
Ser Cys Leu Leu
65
```

```
        <210> 124
        <211> 110
        <212> PRT
        <213> mouse

        <400> 124
```

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1011c2PCTSEQUENCE LISTING

```
Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly
1               5                   10              .       15
Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro
        20                  25                  30
Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser
        35              40                  45
Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
    50                  55                  60
Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys
65                  70                  75                      80
Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
            85                  90                      95
Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His
            100                 105                 110
```

```
                    <210> 125
                    <211> 330
                    <212> PRT
                    <213> mouse


                    <400> 125
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
1               5                   10              15
Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
            20                  25                  30
Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
        35                  40                  45
Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
    50                  55                  60
Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
65                  70                  75                      80
Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
            85                  90                      95
Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
            100                 105                 110
Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
            115                 120                 125
Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
            130                 135                 140
Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
145                 150                 155                     160
Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
            165                 170                 175
Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
            180                 185                 190
Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
            195                 200                 205
Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp
            210                 215                 220
Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp
225                 230                 235                     240
Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro
            245                 250                 255
Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro
            260                 265                 270
```

1011c2PCTSEQUENCE LISTING

```
Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr
    275                 280                 285
Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser
    290                 295                 300
Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu
305                 310                 315                 320
Pro Ser Trp Thr Val Ser Met Asp Thr Gln
                325                 330
```

```
        <210> 126
        <211> 37
        <212> PRT
        <213> Rat


        <400> 126
Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile
1                   5                   10                  15
Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys
                20                  25                  30
Arg Ala Asp Val Leu
        35
```

```
        <210> 127
        <211> 42
        <212> PRT
        <213> mouse


        <400> 127
Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu
1                   5                   10                  15
Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe
                20                  25                  30
Ser Leu His Thr Met Ser Ala Gly Phe Pro
        35                  40
```

```
        <210> 128
        <211> 253
        <212> PRT
        <213> mouse


        <400> 128
Met Met Tyr Trp Ile Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe
1                   5                   10                  15
Thr Asp Ile Phe Ile Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp
                20                  25                  30
Gly Trp Glu Gly Pro His His His His Leu Ala Ser Gly Ser His
        35                  40                  45
Lys Pro Leu Pro Leu Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe
    50                  55                  60
Lys Met Ala Phe Val Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala
65                  70                  75                  80
Ser Leu Leu Tyr Arg Lys Phe Val His Pro Ser Leu Ser Arg His Glu
                85                  90                  95
Lys Glu Ile Asp Ala Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu
            100                 105                 110
```

1011c2PCTSEQUENCE LISTING

Thr Met Leu Ser Phe Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala
        115               120               125
Ala Val Gln Ala Ala Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu
        130               135               140
Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val
145               150                   155               160
Pro Thr Tyr Gln Asp Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg
                165               170               175
Arg Pro Pro Ile Gly Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr
            180               185               190
Glu Asp Glu Cys Trp Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val
        195               200               205
Arg Pro Arg Glu Lys Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val
        210               215               220
Lys Arg Lys Pro Leu Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val
225               230               235               240
Arg Thr Arg Lys Lys Ala Met Pro Ser Asp Met Asp Ser
                245               250

            <210> 129
            <211> 40
            <212> PRT
            <213> mouse


            <400> 129
Met Lys Ala Met Ala Leu Ser Leu Gly Ala Ser Pro Val Leu Ala Phe
1                5               10               15
Leu Leu Ser Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly
            20               25               30
Ser Lys Val Pro Gln Phe Leu Asn
        35               40


            <210> 130
            <211> 87
            <212> PRT
            <213> mouse


            <400> 130
Met Ile Ala Val Thr Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg
1                5               10               15
Ile Ser Thr Ala Ala Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg
            20               25               30
Ser Asn Ile Arg Val Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu
        35               40               45
Val Val Ile Ile Leu Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp
    50               55               60
Leu Thr Lys Ile Gly Glu Cys His Val Gln Asp Ser Ile Gly Ser Met
65               70               75               80
Gly Leu Gly Gln Gly Gln Pro
                85


            <210> 131
            <211> 70
            <212> PRT
            <213> mouse


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1011c2PCTSEQUENCE LISTING

> 131
y Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys
        5                   10              15
l Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro
   20                  25              30
s Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu
                   40                  45
s Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro
                   55                  60
r Leu Ile Ser
           70


> 132
> 63
> PRT
> mouse


> 132
u Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala
        5                   10              15
r Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met
   20                  25              30
s Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly
                   40                  45
u Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu
                   55                  60


> 133
> 39
> PRT
> mouse


> 133
n Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala
        5                   10              15
l Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe
   20                  25              30
p Leu Glu Val Thr


> 134
> 90
> PRT
> Rat


> 134
r Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
        5                   10              15
r Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
   20                  25              30
s Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
                   40                  45
g Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
                   55                  60

1011c2PCTSEQUENCE LISTING

```
<400> 131
Met Phe Gly Leu Val His Val Cys Thr Cys Val Cys Val Cys Val Cys
1               5               10              15
Val Cys Val Cys Val Cys Ile Cys Ser Cys Gly Tyr Val His Val Pro
        20              25              30
Cys Gly Cys Val Cys Leu Trp Gly Pro Glu Val Arg Tyr Leu Pro Leu
        35              40              45
Ser Leu His Pro Gly Gly Phe Cys Phe Val Leu Phe Cys Phe Gly Pro
    50              55              60
Gly Leu Ser Leu Ile Ser
65              70

<210> 132
<211> 63
<212> PRT
<213> mouse

<400> 132
Met Trp Leu Leu Val Ala Leu Thr Leu Ser Val Tyr Ser Leu Val Ala
1               5               10              15
Phe Val Thr Gly Met Leu Cys Asp Thr Val Val Ile Lys Met Leu Met
        20              25              30
Ser Leu His Lys Ser Ser Lys Leu Asn Pro Arg Ala Lys Cys Gly Gly
        35              40              45
Val Pro Leu Ile Pro Ala Leu Trp Gly Gln Val Gln Val Val Leu
    50              55              60

<210> 133
<211> 39
<212> PRT
<213> mouse

<400> 133
Met Asp Asn Thr Leu Ser Ile Ile Ile Tyr Leu Leu Phe Ile Phe Ala
1               5               10              15
Ile Ser Val Leu Asp Ser Gln Leu Ser Thr Arg Cys Leu Trp Trp Phe
        20              25              30
Ser Lys Asp Leu Glu Val Thr
        35

<210> 134
<211> 90
<212> PRT
<213> Rat

<400> 134
Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
1               5               10              15
Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
        20              25              30
Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
        35              40              45
Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
    50              55              60
```

1011c2PCTSEQUENCE LISTING

Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe
65              70              75              80
Ala Gly Glu Val Leu Gly Ile Cys His Ser
                85              90


          <210> 135
          <211> 193
          <212> PRT
          <213> Rat


          <400> 135
Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys
1               5               10              15
Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
            20              25              30
Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
            35              40              45
Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
    50              55              60
Tyr His Ser Phe Val Ser Ser Val Phe Thr Leu Phe Met Ser Arg Thr
65              70              75              80
Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
                85              90              95
Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
            100             105             110
Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
            115             120             125
Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
    130             135             140
Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
145             150             155             160
Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
                165             170             175
Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Met
            180             185             190
Ser


          <210> 136
          <211> 106
          <212> PRT
          <213> Rat


          <400> 136
Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala
1               5               10              15
Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser
            20              25              30
Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln
            35              40              45
Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Leu Asp Ala
    50              55              60
Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val
65              70              75              80
Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr

1011c2PCTSEQUENCE LISTING

```
                     85                        90                       95
Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys
                    100                       105
```

```
        <210> 137
        <211> 286
        <212> PRT
        <213> Rat


        <400> 137
Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu
1               5                   10                  15
Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu
            20                  25                  30
Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala
        35                  40                  45
Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly
    50                  55                  60
Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser
65                  70                  75                      80
Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
                85                  90                  95
Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala
            100                 105                 110
Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser
        115                 120                 125
Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu
    130                 135                 140
Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys
145                 150                 155                     160
Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala
                165                 170                 175
Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys
            180                 185                 190
Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys
        195                 200                 205
Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile
    210                 215                 220
Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu
225                 230                 235                     240
Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly
                245                 250                 255
Lys Lys Glu Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp
            260                 265                 270
Ile Thr Gly Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser
            275                 280                 285


        <210> 138
        <211> 198
        <212> PRT
        <213> Rat


        <400> 138
Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu
1               5                   10                  15
```

1011c2PCTSEQUENCE LISTING

```
Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala
         20                  25                  30
Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro
         35                  40                  45
Gly Pro Gln Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Ser Ser Gly
         50                  55                  60
Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln
65                   70                  75                  80
Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr
             85                  90                  95
Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly
            100                 105                 110
Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys
            115                 120                 125
His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro
            130                 135                 140
Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala
145                 150                 155                 160
Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile
                165                 170                 175
Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser
            180                 185                 190
Ser Gly Lys Phe Val Cys
            195
```

```
<210> 139
<211> 233
<212> PRT
<213> Rat
```

```
<400> 139
Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
1               5                   10                  15
Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
            20                  25                  30
Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
            35                  40                  45
Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
         50                  55                  60
Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
65                   70                  75                  80
Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
             85                  90                  95
Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
            100                 105                 110
Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
            115                 120                 125
Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
            130                 135                 140
Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
145                 150                 155                 160
Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu
                165                 170                 175
Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
            180                 185                 190
```

1011c2PCTSEQUENCE LISTING

Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Met Lys
        195                 200                 205
Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
    210                 215                 220
Glu Asp Thr Glu Phe Leu Gln Pro Gly
225                 230


        <210> 140
        <211> 38
        <212> PRT
        <213> Human

        <400> 140
Met Gly Leu Ala Leu Cys Leu Ala Ser Ala Gly Ile Ser Gly Ser Arg
1                 5                 10                15
Ser Ala Phe Leu Gly Val Pro Arg Pro Arg Pro Thr Leu Ile Lys Leu
            20                25                  30
Ile Asp Thr Val Asp Leu
        35


        <210> 141
        <211> 322
        <212> PRT
        <213> mouse

        <400> 141
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
1                 5                 10              15
Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
            20                25                  30
Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
        35                40                  45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
    50                  55                60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65                  70                75                80
Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
                85                90                  95
Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
            100               105                 110
Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
        115               120                 125
Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
        130               135                 140
Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145               150                 155                 160
Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
                165               170                 175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
            180               185                 190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
        195               200                 205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
    210               215                 220
Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

1011c2PCTSEQUENCE LISTING

```
225                    230                    235                    240
Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                245                    250                    255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
                260                    265                    270
Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
                275                    280                    285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
                290                    295                    300
Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305                    310                    315                    320
Gln Gly
```

```
<210> 142
<211> 312
<212> PRT
<213> mouse

<400> 142
Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr
1                    5                    10                   15
Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser
                20                   25                   30
Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr
                35                   40                   45
Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp
        50                   55                   60
Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu
65                   70                   75                   80
Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly
                85                   90                   95
Arg Ile Asp Ala Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val
                100                  105                  110
Lys Ile Ser Glu Gln Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys
        115                  120                  125
Asn Gly Thr Met Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu
        130                  135                  140
Leu His Pro Val Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His
145                  150                  155                  160
Ser Thr Ile Phe Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe
                165                  170                  175
Thr Val Glu Glu Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala
        180                  185                  190
Gly Gly Gly Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp
        195                  200                  205
Arg Leu Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met
210                  215                  220
Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys
225                  230                  235                  240
Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu
                245                  250                  255
Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly
                260                  265                  270
Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser
```

1011c2PCTSEQUENCE LISTING

```
            275                     280                    285
Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu
       290                     295                    300
Lys Thr Arg Met Ala Leu Arg Lys
305                     310
```

        <210> 143
        <211> 163
        <212> PRT
        <213> Rat

        <400> 143

```
Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr
1               5                   10                  15
Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe
            20                  25                  30
Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala
        35                  40                  45
Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn
        50                  55                  60
Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val
65                  70                  75                  80
Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu
                85                  90                  95
Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr
            100                 105                 110
Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys
        115                 120                 125
Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser
        130                 135                 140
Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg
145                 150                 155                 160
Trp Lys Asn
```

        <210> 144
        <211> 330
        <212> PRT
        <213> Rat

        <400> 144

```
Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
1               5                   10                  15
Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu
            20                  25                  30
Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
        35                  40                  45
Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
        50                  55                  60
Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
65                  70                  75                  80
Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
                85                  90                  95
Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
            100                 105                 110
```

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1011c2PCTSEQUENCE LISTING

Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
        115                 120                 125
Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
        130                 135                 140
Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
145                 150                 155                 160
Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
                165                 170                 175
Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
                180                 185                 190
Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
        195                 200                 205
Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
        210                 215                 220
Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
225                 230                 235                 240
Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
                245                 250                 255
Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
                260                 265                 270
Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
        275                 280                 285
Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
        290                 295                 300
Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
305                 310                 315                 320
His Arg Lys Ala Phe Leu Pro Phe Leu Phe
                325                 330

        <210> 145
        <211> 301
        <212> PRT
        <213> Rat

        <400> 145
Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
1                 5                 10                 15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
        20                 25                 30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
        35                 40                 45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
50                 55                 60
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
65                 70                 75                 80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
                85                 90                 95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
                100                 105                 110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
        115                 120                 125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
        130                 135                 140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
145                 150                 155                 160

1011c2PCTSEQUENCE LISTING

```
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
                165             170             175
Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
            180             185             190
Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
        195             200             205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
    210             215             220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
225             230             235             240
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
            245             250             255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
            260             265             270
Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
            275             280             285
Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
290             295             300
```

```
        <210> 146
        <211> 61
        <212> PRT
        <213> Rat
```

```
        <400> 146
Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
1               5               10              15
His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
            20              25              30
Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
        35              40              45
Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
    50              55              60
```

```
        <210> 147
        <211> 105
        <212> PRT
        <213> Rat
```

```
        <400> 147
Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
1               5               10              15
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
            20              25              30
Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
            35              40              45
Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile
    50              55              60
Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu
65              70              75              80
Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly
            85              90              95
Glu Arg Gly Gln His Gly Pro Lys Gly
            100             105
```

1011c2PCTSEQUENCE LISTING

```
        <210> 148
        <211> 210
        <212> PRT
        <213> Rat


        <400> 148
Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val
1               5               10              15
Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu
            20              25              30
Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile Phe Tyr Ser
        35              40              45
Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile
    50              55              60
Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Leu Pro Arg Leu Pro His
65              70              75              80
Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser
            85              90              95
Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr
            100             105             110
His Leu Gln Thr Pro Leu Gln Ala Trp Arg Thr Arg Ala Lys Leu Pro
        115             120             125
Pro Gly Gly Thr Glu Ala Val Pro Gly Arg Pro Gly Ala Gln Gln Asp
    130             135             140
Ala Cys His Leu Leu Tyr Trp Thr Tyr Asn Gly Val Ser Ser Ile Pro
145             150             155             160
Cys His Arg Gly Gly Leu Ser His Val Pro Ser Glu Val Pro Ala Glu
            165             170             175
Lys Ser Pro Val Leu Ile Leu His Ala Ala Pro Pro Phe Lys Thr Pro
            180             185             190
Val Asn Pro Trp Ala Arg Thr Val Val Gly Phe Phe Pro Ser Ser Pro
        195             200             205
Ser Leu
    210


        <210> 149
        <211> 301
        <212> PRT
        <213> Rat


        <400> 149
Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
1               5               10              15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
            20              25              30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
        35              40              45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
    50              55              60
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
65              70              75              80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
            85              90              95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
            100             105             110
```

1011c2PCTSEQUENCE LISTING

```
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
        115                 120                 125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
    130                 135                 140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
145                 150                 155                 160
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
            165                 170                 175
Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
            180                 185                 190
Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
        195                 200                 205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
    210                 215                 220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
225                 230                 235                 240
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
            245                 250                 255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
            260                 265                 270
Gln Arg Cys Leu Leu Gly Leu Pro Val Trp Glu Gly Ser Pro His Leu
    275                 280                 285
Pro Thr Gly His Trp Leu Arg Glu Leu Trp Ser Leu Leu
    290                 295                 300
```

        <210> 150
        <211> 80
        <212> PRT
        <213> Human

        <400> 150
```
Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
1                 5                 10                  15
Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
            20                  25                  30
Phe Gln Asp Thr Lys Val Tyr Cys Thr Arg Glu Ser Asn Pro His Cys
        35                  40                  45
Gly Ser Asp Gly Gln Thr Tyr Gly Asn Lys Cys Ala Phe Cys Lys Ala
    50                  55                  60
Ile Val Lys Ser Gly Gly Lys Ile Ser Leu Lys His Pro Gly Lys Cys
65                  70                  75                  80
```

        <210> 151
        <211> 27
        <212> PRT
        <213> mouse

        <400> 151
```
Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
1                 5                 10                  15
Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
            20                  25
```

        <210> 152
        <211> 86

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1011c2PCTSEQUENCE LISTING

```
        <212> PRT
        <213> mouse

        <400> 152
Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
1               5               10              15
Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
            20              25              30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
        35              40              45
Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly
        50              55              60
Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp
65              70              75              80
Leu Leu Ser Phe Pro Pro
                85


        <210> 153
        <211> 72
        <212> PRT
        <213> mouse

        <400> 153
Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu
1               5               10              15
Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu
            20              25              30
Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg
        35              40              45
Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met
        50              55              60
Ala Phe Ser Ile Leu Phe Ile Gln
65                  70


        <210> 154
        <211> 169
        <212> PRT
        <213> mouse

        <400> 154
Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
1               5               10              15
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
            20              25              30
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
            35              40              45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
        50              55              60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
65                  70              75              80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
            85              90              95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
            100             105             110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
```

1011c2PCTSEQUENCE LISTING

```
            115                      120                    125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
        130                      135                    140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
145                      150                    155             160
Gly Glu Met Pro Pro Glu Asp Gly Met
                165
```

```
        <210> 155
        <211> 61
        <212> PRT
        <213> mouse
```

```
        <400> 155
Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile
1                 5                 10                    15
Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val
            20                  25                    30
Thr Val Thr Gln Met Arg Thr Ile Ile Ile Thr Met Asp Gln Leu Arg
        35                      40                    45
Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser
        50                  55                    60
```

```
        <210> 156
        <211> 131
        <212> PRT
        <213> mouse
```

```
        <400> 156
Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala
1                 5                 10                    15
Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg
            20                  25                    30
Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln
        35                      40                    45
Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala
        50                  55                    60
Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr
65                      70                      75              80
Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg
            85                      90                    95
Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
            100                    105                  110
Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
        115                    120                    125
Leu Arg Arg
        130
```

```
        <210> 157
        <211> 133
        <212> PRT
        <213> mouse
```

```
        <400> 157
Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Cys
```

1011c2PCTSEQUENCE LISTING

```
1                   5                        10                      15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
            20                      25                      30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
        35                      40                      45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Glu His Val
        50                      55                      60
Gln Gly Thr Gly Ala Arg Ser Thr Ala Cys Thr Leu Ser Cys Arg Ala
65                      70                      75                      80
Pro Asn Ala Ser Ser Ser Gly Thr Met Pro Gly Thr Arg Ser Ala Gly
                85                      90                      95
Ser Thr Lys Asn Arg Val Asp Asp His Gly Lys Lys Asn Ser Arg Pro
                100                     105                     110
Val Glu Arg Leu Gln Gln Arg Thr Leu Gln Ile Lys Ile Lys Ala Leu
            115                     120                     125
Ser Phe Ser Gln Ala
        130
```

```
        <210> 158
        <211> 78
        <212> PRT
        <213> mouse


        <400> 158
Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
1                   5                        10                      15
Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
            20                      25                      30
Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
        35                      40                      45
Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
        50                      55                      60
Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
65                      70                      75
```

```
        <210> 159
        <211> 206
        <212> PRT
        <213> mouse


        <400> 159
Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
1                   5                        10                      15
Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
            20                      25                      30
Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser
        35                      40                      45
Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
        50                      55                      60
Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
65                      70                      75                      80
Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
                85                      90                      95
Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
                100                     105                     110
```

1011c2PCTSEQUENCE LISTING

```
Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser
        115             120             125
Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln
        130             135             140
Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val
145             150             155             160
Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser
                165             170             175
His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg
        180             185             190
Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser
        195             200             205
```

```
        <210> 160
        <211> 169
        <212> PRT
        <213> mouse


        <400> 160
Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
1               5               10              15
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
        20              25              30
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
        35              40              45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
        50              55              60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
65              70              75              80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
                85              90              95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
        100             105             110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
        115             120             125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
        130             135             140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
145             150             155             160
Gly Glu Met Pro Pro Glu Asp Gly Met
                165
```

```
        <210> 161
        <211> 114
        <212> PRT
        <213> mouse


        <400> 161
Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu
1               5               10              15
Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp
        20              25              30
Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu
        35              40              45
Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile
```

1011c2PCTSEQUENCE LISTING

```
                50                    55                    60
His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
65                    70                    75                    80
Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
                85                    90                    95
Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
                100                   105                   110
Ser Leu
```

<210> 162
<211> 46
<212> PRT
<213> mouse

<400> 162
```
Met His Tyr Pro Cys Leu Ala Cys Leu Phe Val Asn Val His Trp Cys
1                   5                   10                    15
Phe Ala Trp Met Cys Ile Leu Val Lys Met Ser Glu Leu Leu Glu Leu
                20                    25                    30
Glu Leu Glu Thr Met Val Ser Cys Leu Val Asp Val Gly Asn
        35                    40                    45
```

<210> 163
<211> 122
<212> PRT
<213> mouse

<400> 163
```
Met Phe Thr Phe Val Val Leu Val Ile Thr Ile Val Ile Cys Leu Cys
1                   5                   10                    15
His Val Cys Phe Gly His Phe Lys Tyr Leu Ser Ala His Asn Tyr Lys
                20                    25                    30
Ile Glu His Thr Glu Thr Asp Ala Val Ser Ser Arg Ser Asn Gly Arg
        35                    40                    45
Pro Pro Thr Ala Gly Ala Val Pro Lys Ser Ala Lys Tyr Ile Ala Gln
    50                    55                    60
Val Leu Gln Asp Ser Glu Gly Asp Gly Asp Gly Ala Pro Gly
65                    70                    75                    80
Ser Ser Gly Asp Glu Pro Pro Ser Ser Ser Ser Gln Asp Glu Glu Leu
                85                    90                    95
Leu Met Pro Pro Asp Gly Leu Thr Asp Thr Asp Phe Gln Ser Cys Glu
                100                   105                   110
Asp Ser Leu Ile Glu Asn Glu Ile His Gln
        115                   120
```

<210> 164
<211> 60
<212> PRT
<213> Rat

<400> 164
```
Met Ser Phe Val Lys Ile Glu Ala Thr Pro Thr Gln Thr Lys Trp Pro
1                   5                   10                    15
Phe Ser Val Val Pro Gln Ser Leu Leu Val Thr Val Tyr Ile Cys Tyr
```

1011c2PCTSEQUENCE LISTING
```
            20                      25                      30
Ile Phe Leu Val Ile Phe Phe Phe Phe Glu Ala Cys Gln Glu Val
            35                      40                      45
Leu Cys Ser Phe Phe Asp Phe Ser Arg Arg Arg Gly
            50                      55                      60
```

        <210> 165
        <211> 57
        <212> PRT
        <213> mouse

        <400> 165
```
Met Gly Ser Pro Ile Ser Gly Val Cys Pro Val Leu Pro Gly Gly Leu
1               5                   10                      15
Phe Val Ala Leu Gly Trp Ile Phe Leu Leu Phe His Arg Asp Ala Phe
            20                      25                      30
Ser Leu His Thr Met Ser Ala Gly Phe Pro Lys Ser Pro Ala Asn Pro
            35                      40                      45
His His Pro Pro Leu Arg Leu Ser Pro
            50                      55
```

        <210> 166
        <211> 75
        <212> PRT
        <213> mouse

        <400> 166
```
Lys Thr Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp
1               5                   10                      15
Phe Met Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro
            20                      25                      30
Phe Pro Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys
            35                      40                      45
Gln Trp Glu Gly Ser Thr Met Thr His Thr His Thr His Thr His Ile
            50                      55                      60
His Ile His Thr Pro Pro Arg Gln Cys Gln Ser
65                      70                      75
```

        <210> 167
        <211> 52
        <212> PRT
        <213> mouse

        <400> 167
```
Val Arg Ser Leu Glu Gln Leu Gly Leu Phe Ser Val Asp Phe Met Val
1               5                   10                      15
Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro Phe Pro Leu
            20                      25                      30
Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys Gln Trp Glu
            35                      40                      45
Gly Ser Thr Met
            50
```

        <210> 168
        <211> 119
```

1011c2PCTSEQUENCE LISTING

```
<212> PRT
<213> Rat

<400> 168
Met Leu Gly Ala Thr Ser Leu Ser Trp Pro Trp Val Leu Trp Ala Val
1           5                   10                  15
Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu Gly Gly Leu
            20                  25                  30
Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile Phe Tyr Ser
        35                  40                  45
Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly Met Ala Ile
        50                  55                  60
Phe Ser Leu Leu Leu Gln Ala Leu Leu Leu Pro Arg Leu Pro His
65                  70                  75                  80
Ala Pro Gly Ser Glu Gly Val Ser Ser Arg Ser Ala Arg Ile Ser Ser
                85                  90                  95
Asp Leu Leu Arg Asn Ile Val Pro Thr Arg Gln Leu Thr Arg Gln Thr
            100                 105                 110
His Leu Gln Thr Pro Leu Gln
        115

<210> 169
<211> 104
<212> PRT
<213> Rat

<220>

<400> 169
Leu Val Pro Lys Ser Ala Arg Ala Ser Leu Leu Cys Cys Gly Pro Lys
1           5                   10                  15
Leu Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu
            20                  25                  30
Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Xaa Ile Xaa
        35                  40                  45
Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile
        50                  55                  60
Tyr Asn Leu Tyr Glu Gln Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly
65                  70                  75                  80
Leu Tyr Leu Leu Xaa Gly Gly Phe Ser Phe Cys Gln Val Arg Leu Asn
                85                  90                  95
Lys Arg Lys Glu Tyr Met Val Arg
            100

<210> 170
<211> 123
<212> PRT
<213> Rat

<220>
<221> UNSURE
<222> (27)...(27)

<221> UNSURE
```

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1011c2PCTSEQUENCE LISTING
```
<222> (104)...(104)

<221> UNSURE
<222> (118)...(118)

<400> 170
Met Arg Pro Gly Ala Asp Trp Ala Ala Val Cys Ala Leu Trp Pro Ser
1               5                   10                  15
Trp Arg Pro Ser Cys Ser Leu Pro Ser Ser Xaa Arg Ile Gln Pro Asp
            20                  25                  30
Glu Leu Trp Leu Tyr Arg Asn Pro Tyr Val Lys Ala Glu Tyr Phe Pro
        35                  40                  45
Thr Gly Pro Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile
    50                  55                  60
Phe Phe Ala Lys Phe Leu Arg Lys Ala Asp Ala Asp Arg Gln Arg Ala
65                  70                  75                  80
Ser Leu Pro Arg Cys Gln Pro Cys Pro Ser Ala Lys Trp Cys Leu Tyr
            85                  90                  95
Gln His His Lys Thr Asp Ser Xaa Gln Gly His Ala Gln Ile Ala Ser
            100                 105                 110
Thr Glu Cys Ser Pro Xaa Gly Ile Ala His Ser
    115                 120
```

```
<210> 171
<211> 75
<212> PRT
<213> Rat

<400> 171
Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
1               5                   10                  15
Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
            20                  25                  30
Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
        35                  40                  45
Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
    50                  55                  60
Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
65                  70                  75
```

```
<210> 172
<211> 79
<212> PRT
<213> Human

<400> 172
Lys Thr Ser Tyr His Tyr His Thr Asn Val Glu Glu Leu Thr Ile Pro
1               5                   10                  15
Glu Thr Arg Asn Asn Leu Tyr Ile Ser Ile Ser Trp Leu Trp Cys Leu
            20                  25                  30
Val Leu Val Leu Leu Ser Thr Met Ile Leu Asn Lys His Gly Trp Met
        35                  40                  45
Lys Ala Asn Ala Tyr Ser Leu Val Pro Ser Ile Ile Tyr Ser Pro Ser
    50                  55                  60
Tyr Leu Lys Leu Leu Leu Arg Leu Tyr Lys Leu Gln Ile Cys Cys
```

1011c2PCTSEQUENCE LISTING
65                         70                        75

```
        <210> 173
        <211> 134
        <212> PRT
        <213> Human

        <220>
<400> 173
Leu Arg Gly Arg Gly Arg Gly Val Cys Ser Gln Glu Ser Phe Gly Gly
1               5                   10                  15
Cys Cys Val Ser Gly Leu Ile Ala Met Gly Thr Lys Ala Gln Val Glu
            20                  25                  30
Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Leu Cys Ser Leu
            35                  40                  45
Ala Leu Gly Ser Val Thr Val His Ser Ser Glu Pro Glu Val Arg Ile
        50                  55                  60
Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser
65                  70                  75                  80
Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu
                85                  90                  95
Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr
            100                 105                 110
Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr
            115                 120                 125
Gly Thr Tyr Thr Cys Met
        130

        <210> 174
        <211> 137
        <212> PRT
        <213> Human

        <400> 174
Ala Trp Ser Arg Pro Arg Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala
1               5                   10                  15
Leu Gln Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe
            20                  25                  30
Leu Ala Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly
            35                  40                  45
Gly Asp Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile
        50                  55                  60
Ile Phe Ile Val Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr
65                  70                  75                  80
Gly His Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn
                85                  90                  95
Ile Lys Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser
            100                 105                 110
Ala Leu Val Ile Leu Gly Gly Ala Leu Ser Pro Val Pro Val Leu Gly
            115                 120                 125
Ile Arg Ala Gly Leu Gly Thr Cys Pro
        130                 135

        <210> 175
        <211> 43
```

1011c2PCTSEQUENCE LISTING

```
       <212> PRT
       <213> Human

       <400> 175
Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
1               5                  10                  15
Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
           20                  25                  30
Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn
       35                  40


       <210> 176
       <211> 63
       <212> PRT
       <213> Rat


       <400> 176
Pro Asn Thr Arg Pro Arg Arg His Thr Ala Cys Arg Val Ser Ile Ser
1               5                  10                  15
Val Phe Tyr Met Leu His Thr Glu Leu Lys Lys Cys Trp Phe Phe Leu
           20                  25                  30
Phe Cys Phe Ser Leu Phe Leu Trp Phe Cys Phe Trp Phe Cys Phe Leu
           35                  40                  45
Leu Pro Arg Phe Asp Tyr Leu Pro Met Pro Ser Thr Arg Pro Arg
   50                  55                  60


       <210> 177
       <211> 52
       <212> PRT
       <213> mouse


       <400> 177
Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
1               5                  10                  15
Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
           20                  25                  30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
       35                  40                  45
Gly Ala Gln Gly
   50


       <210> 178
       <211> 62
       <212> PRT
       <213> mouse


       <400> 178
Val Ser Pro Arg Pro Thr Tyr Pro Ser Thr Ala Ser Ser Met Ala Ala
1               5                  10                  15
Phe Leu Val Thr Gly Phe Phe Phe Ser Leu Phe Val Val Leu Gly Met
           20                  25                  30
Glu Pro Arg Ala Leu Phe Arg Pro Asp Lys Ala Leu Pro Leu Ser Cys
       35                  40                  45
Ala Lys Pro Thr Ser Leu Cys Val Gln Ser Ser Phe Leu Gly
   50                  55                  60
```

1011c2PCTSEQUENCE LISTING

```
        <210> 179
        <211> 123
        <212> PRT
        <213> mouse


        <400> 179
Ala Ser Arg Thr Ala Val Met Ser Leu Cys Arg Cys Gln Gln Gly Ser
1               5                   10                  15
Arg Ser Arg Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly
            20                  25                  30
Gly Thr Leu Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu
        35                  40                  45
Trp Pro Ser Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr
    50                  55                  60
Leu Gly Met Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys
65                  70                  75                  80
Tyr Ser Phe Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu
            85                  90                  95
His Gly Phe Ser Ala His Lys Gly His Val Ala Gln Arg Gly Gln Val
            100                 105                 110
Pro Ser Arg Lys Asn Leu His Phe Gly Cys Val
        115                 120
```

```
        <210> 180
        <211> 120
        <212> PRT
        <213> mouse

        <220>
        <221> UNSURE
        <222> (5)...(5)

        <400> 180
Ala Arg Arg Arg Xaa Arg Trp Arg Arg Gly Cys Cys Trp Leu Ile Gly
1               5                   10                  15
Thr Gly Leu Arg Ala Ala Thr Trp Thr Val Leu Cys Ser Pro Asn Ser
            20                  25                  30
Ser Leu Val Val Ala Arg His Thr Lys Ser Phe Pro Pro Lys Lys Pro
        35                  40                  45
Leu Gln Ala Leu Thr Met Ser Ile Met Asp His Ser Pro Thr Thr Gly
    50                  55                  60
Val Val Thr Val Ile Val Ile Leu Ile Ala Ile Ala Ala Leu Gly Gly
65                  70                  75                  80
Leu Ile Leu Gly Cys Trp Cys Tyr Leu Arg Leu Gln Arg Ile Ser Gln
            85                  90                  95
Ser Glu Asp Glu Glu Ser Ile Val Gly Asp Gly Glu Thr Lys Glu Pro
            100                 105                 110
Phe Tyr Trp Cys Ser Thr Leu Leu
        115                 120
```

```
        <210> 181
        <211> 60
        <212> PRT
        <213> mouse
```

1011c2PCTSEQUENCE LISTING

```
          <400> 181
Lys Gly Pro Glu Val Ser Cys Cys Ile Lys Tyr Phe Ile Phe Gly Phe
 1               5               10               15
Asn Val Ile Phe Trp Phe Leu Gly Ile Thr Phe Leu Gly Ile Gly Leu
             20               25               30
Trp Ala Trp Asn Glu Lys Gly Val Leu Ser Asn Ile Ser Ser Ile Thr
         35               40               45
Asp Leu Gly Gly Phe Asp Pro Val Trp Leu Phe Leu
     50               55               60
```

```
          <210> 182
          <211> 72
          <212> PRT
          <213> mouse

          <220>
```

```
          <400> 182
Lys Pro Thr Val Gly Ser Ala Glu Val Ala Ile Ala Val Phe Leu Val
 1               5               10               15
Ile Cys Ile Ile Val Val Leu Thr Ile Leu Gly Tyr Cys Phe Phe Lys
             20               25               30
Asn Gln Arg Lys Glu Phe His Ser Pro Leu His His Pro Pro Pro Thr
         35               40               45
Pro Ala Ser Ser Thr Val Ser Thr Thr Glu Asp Thr Glu His Leu Val
     50               55               60
Tyr Asn His Thr Thr Gln Pro Leu
65               70
```

```
          <210> 183
          <211> 771
          <212> PRT
          <213> Rat

          <220>
```

```
          <400> 183
Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu Leu
 1               5               10               15
Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg Ile
             20               25               30
Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu Thr
         35               40               45
Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr Phe
     50               55               60
Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp Ile
65               70               75               80
Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu Ser Ala Leu Ser His
             85               90               95
Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln Trp
            100              105              110
Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala Arg
```

1011c2PCTSEQUENCE LISTING

```
         115                          120                      125
Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr Pro
    130                      135                  140
Ser Lys Asn Phe Thr Cys Gln Gly Pro Val Asp Val Thr Ile Gln Ala
145                      150                  155                  160
Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr Cys
                 165                  170                  175
Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly Phe
             180                  185                  190
Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Thr Ser Asn Pro
         195                  200                  205
Cys Lys His Gly Gly Thr Cys His Leu Lys Pro Arg Arg Glu Thr Trp
    210                  215                  220
Ile Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly Glu Ser Cys Asp Ile
225                  230                  235                  240
Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr Cys
                 245                  250                  255
Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr Thr
             260                  265                  270
Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu Asn
         275                  280                  285
Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe Lys
    290                  295                  300
Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His Cys Asp Ile Asp Phe
305                  310                  315                  320
Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr Asp
                 325                  330                  335
Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu Gly Tyr Ser Gly Leu
             340                  345                  350
Phe Cys Glu Phe Ser Pro Pro Met Val Phe Leu Arg Thr Ser Pro Cys
         355                  360                  365
Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Ile Arg Val Asn
    370                  375                  380
Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu Gly Glu Lys Cys Glu
385                  390                  395                  400
Lys Leu Val Ser Val Ser Ile Leu Val Asn Lys Glu Ser Tyr Leu Gln
                 405                  410                  415
Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile
             420                  425                  430
Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys Gly Asp Lys Asp
         435                  440                  445
His Ile Ala Val Glu Ser Ile Glu Gly Ile Arg Ala Ser Tyr Asp Thr
    450                  455                  460
Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val Glu Thr Ile Asn Asp
465                  470                  475                  480
Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu Asp Ser Ser Leu Ser
                 485                  490                  495
Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile Thr Asn Leu Ser Lys
             500                  505                  510
Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr Val Gly Gly Met Pro
         515                  520                  525
Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala Pro Gly Gln Asn Gly
    530                  535                  540
Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr Ile Asn Ser Glu Leu
545                  550                  555                  560
```

1011c2PCTSEQUENCE LISTING

```
Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly Ile Leu Pro Gly Cys
            565             570             575
Glu Pro Cys His Lys Lys Val Cys Ala His Gly Thr Cys Gln Pro Ser
            580             585             590
Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu Gly Trp Met Gly Pro
            595             600             605
Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu Gly Asn Lys Cys Val
    610             615             620
His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser Tyr Ser Cys Lys Cys
625             630             635             640
Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu Glu Glu Asp Leu Phe
            645             650             655
Asn Pro Leu Pro Gly Asp Gln Val Gln Ala Arg Glu Val Gln Ala Leu
            660             665             670
Trp Ala Arg Ala Ala Leu Leu Trp Met Gln Gln Trp Ile His Arg Gly
            675             680             685
Gln Leu Thr Gln Arg Ile Ser Cys Arg Gly Glu Arg Ile Arg Asp Tyr
            690             695             700
Tyr Gln Ser Ser Arg Val Arg Cys Leu Ser Asn Asp


            <210> 184
            <211> 340
            <212> PRT
            <213> mouse


            <400> 184
Asp Gly Ser Leu Trp Leu Gln Ala Thr Gln Pro Asp Asp Ala Gly His
1               5               10              15
Tyr Thr Cys Val Pro Ser Asn Gly Phe Leu His Pro Pro Ser Ala Ser
            20              25              30
Ala Tyr Leu Thr Val Leu Tyr Pro Ala Gln Val Thr Val Met Pro Pro
            35              40              45
Glu Thr Pro Leu Pro Thr Gly Met Arg Gly Val Ile Arg Cys Pro Val
    50              55              60
Arg Ala Asn Pro Pro Leu Leu Phe Val Thr Trp Thr Lys Asp Gly Gln
65              70              75              80
Ala Leu Gln Leu Asp Lys Phe Pro Gly Trp Ser Leu Gly Pro Glu Gly
            85              90              95
Ser Leu Ile Ile Ala Leu Gly Asn Glu Asp Ala Leu Gly Glu Tyr Ser
            100             105             110
Cys Thr Pro Tyr Asn Ser Leu Gly Thr Ala Gly Pro Ser Pro Val Thr
            115             120             125
Arg Val Leu Leu Lys Ala Pro Pro Ala Phe Ile Asp Gln Pro Lys Glu
    130             135             140
Glu Tyr Phe Gln Glu Val Gly Arg Glu Leu Leu Ile Pro Cys Ser Ala
145             150             155             160
Arg Gly Asp Pro Pro Pro Ile Val Ser Trp Ala Lys Val Gly Arg Gly
            165             170             175
Leu Gln Gly Gln Ala Gln Val Asp Ser Asn Asn Ser Leu Val Leu Arg
            180             185             190
Pro Leu Thr Lys Glu Ala Gln Gly Arg Trp Glu Cys Ser Ala Ser Asn
            195             200             205
Ala Val Ala Arg Val Thr Thr Ser Thr Asn Val Tyr Val Leu Gly Thr
    210             215             220
Ser Pro His Val Val Thr Asn Val Ser Val Val Pro Leu Pro Lys Gly
```

1011c2PCTSEQUENCE LISTING

```
225                    230                    235                    240
Ala Asn Val Ser Trp Glu Pro Gly Phe Asp Gly Gly Tyr Leu Gln Arg
                245                    250                    255
Phe Ser Val Trp Tyr Thr Pro Leu Ala Lys Arg Pro Asp Arg Ala His
                260                    265                    270
His Asp Trp Val Ser Leu Ala Val Pro Ile Gly Ala Thr His Leu Leu
                275                    280                    285
Val Pro Gly Leu Gln Ala His Ala Gln Tyr Gln Phe Ser Val Leu Ala
                290                    295                    300
Gln Asn Lys Leu Gly Ser Gly Pro Phe Ser Glu Ile Val Leu Ser Ile
305                    310                    315                    320
Pro Glu Gly Leu Pro Thr Thr Pro Ala Ala Pro Gly Leu Pro Ala Thr
                325                    330                    335
Arg Ser Arg Val
                340


        <210> 185
        <211> 536
        <212> PRT
        <213> mouse


        <400> 185
Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
1                   5                    10                     15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
                20                     25                     30
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
                35                     40                     45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
        50                     55                     60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
65                     70                     75                     80
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
                85                     90                     95
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
                100                    105                    110
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
                115                    120                    125
Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp
        130                    135                    140
Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr Gln Met Ser Arg
145                    150                    155                    160
Phe Leu Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His
                165                    170                    175
Asp Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Gly Tyr Leu Pro Pro
                180                    185                    190
Glu Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val
                195                    200                    205
Tyr Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Asn Asn Pro
        210                    215                    220
Phe Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys
225                    230                    235                    240
Gly His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala
                245                    250                    255
Cys Ala Ser Leu Ile Gly Leu Met Gln Arg Cys Trp His Ala Asp Pro
```

1011c2PCTSEQUENCE LISTING

```
         260                      265                      270
Gln Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu
     275                      280                      285
Cys Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly
     290                      295                      300
Glu Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser
305                      310                      315                      320
Arg Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu
                 325                      330                      335
Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Phe Pro Arg Leu Leu
             340                      345                      350
Lys Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro
         355                      360                      365
Ser Ser Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser
     370                      375                      380
Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala
385                      390                      395                      400
Ser Thr Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val
                 405                      410                      415
Asp Ala Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln
             420                      425                      430
Pro Gln Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His
         435                      440                      445
Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu
     450                      455                      460
Asn Asn Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu
465                      470                      475                      480
His Met Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu
                 485                      490                      495
Ala Arg Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala
             500                      505                      510
Leu His Phe Ala Ala Gln Asn Gly Asp Glu Gly Gln His Lys Ala Ala
         515                      520                      525
Ala Arg Glu Glu Cys Phe Cys Gln
         530                      535
```

```
    <210> 186
    <211> 337
    <212> PRT
    <213> Rat

    <220>


    <400> 186
Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp
 1               5                    10                      15
    Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile
                 20                      25                      30
    Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr
             35                      40                      45
    Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly
         50                      55                      60
    Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr
    65                      70                      75                      80
```

1011c2PCTSEQUENCE LISTING

```
Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp
             85            90               95
Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn
         100             105             110
Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu
         115             120             125
Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu
     130             135             140
Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys
145             150             155             160
Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser Cys Gln
             165             170             175
Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro Leu Gln
         180             185             190
Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Val
         195             200             205
Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met Cys Pro
     210             215             220
Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Phe Arg
225             230             235             240
Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln
             245             250             255
Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile
         260             265             270
Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro
         275             280             285
Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp
         290             295             300
Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe
305             310             315             320
Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro
             325             330             335
Phe
```

```
<210> 187
<211> 152
<212> PRT
<213> mouse

<400> 187
Met Ala Leu Gly Val Leu Ile Ala Val Cys Leu Leu Phe Lys Ala Met
1             5               10              15
Lys Ala Ala Leu Ser Glu Glu Ala Glu Val Ile Pro Pro Ser Thr Ala
         20              25              30
Gln Gln Ser Asn Trp Thr Phe Asn Asn Thr Glu Ala Asp Tyr Ile Glu
         35              40              45
Glu Pro Val Ala Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn
     50              55              60
Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln
65              70              75              80
Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His
             85              90              95
Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile Ala
         100             105             110
```

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1011c2PCTSEQUENCE LISTING

```
Ile Gly Ile Gly Val Gly Leu Leu Ile Ser Ala Phe Leu Ala Val Phe
        115             120             125
Tyr Cys Tyr Ile Arg Lys Arg Cys Ile Asn Leu Lys Ser Pro Tyr Ile
        130             135             140
Ile Cys Ser Gly Gly Ser Pro Leu
145             150
```

```
        <210> 188
        <211> 118
        <212> PRT
        <213> Rat

        <220>


        <400> 188
Leu Val Pro Gln Phe Gly Thr Arg Ile Arg Tyr ThrAla Tyr Asp Arg
  1             5             10              15
Ala Tyr Asn Arg Ala Ser Cys Lys Phe Ile Val Lys Val Gln Val Arg
        20             25             30
Arg Cys Pro Ile Leu Lys Pro Pro Gln His Gly Tyr Leu Thr Cys Ser
        35             40             45
Ser Ala Gly Asp Asn Tyr Gly Ala Ile Cys Glu Tyr His Cys Asp Gly
        50             55             60
Gly Tyr Glu Arg Gln Gly Thr Pro Ser Arg Val Cys Gln Ser Ser Arg
65             70             75             80
Gln Trp Ser Gly Ser Pro Pro Val Cys Thr Pro Met Lys Ile Asn Val
        85             90             95
Asn Val Asn Ser Ala Ala Gly Leu Leu Asp Gln Phe Tyr Glu Lys Gln
        100            105            110
Arg Leu Leu Ile Val Ser
        115
```

```
        <210> 189
        <211> 299
        <212> PRT
        <213> Human

        <220>


        <400> 189
Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1             5             10              15
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
        20             25             30
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
        35             40             45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
        50             55             60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65             70             75             80
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
        85             90             95
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
        100            105            110
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
```

1011c2PCTSEQUENCE LISTING

```
           115                         120                      125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
   130                     135                  140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
145                     150                  155                  160
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
               165                  170                  175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
           180                  185                  190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
           195                  200                  205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
   210                     215                  220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225                     230                  235                  240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
               245                  250                  255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
           260                  265                  270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
           275                  280                  285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
           290                  295
```

```
           <210> 190
           <211> 91
           <212> PRT
           <213> Human


           <400> 190
Gln Pro Thr Val Phe Trp Pro Lys Thr Ser Ala Lys Lys Gly Asn Trp
1                   5                   10                  15
Val Leu Arg Leu Gly Leu Ser Asn Pro Asp Arg Pro Ala Arg Gln Asn
               20                  25                  30
Asn Trp Phe Leu Pro Ala Ser Arg Glu Ile Pro Glu His Ser Ala Leu
           35                  40                  45
Thr Arg Tyr Pro Ala Gln Ile Arg Gly Cys Trp Pro His Arg Leu Thr
       50                  55                  60
Lys Pro Gln Thr Cys Leu Pro Gln Ala Arg Ser Tyr Leu Ser His Glu
65                  70                  75                  80
Val Thr Gln Ala Thr Arg Thr Cys Pro Gly Gly
               85                  90
```

```
           <210> 191
           <211> 89
           <212> PRT
           <213> mouse


           <400> 191
Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu Asp
1                   5                   10                  15
Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly Lys
               20                  25                  30
Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr Ala
           35                  40                  45
```

1011c2PCTSEQUENCE LISTING
```
Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr Pro
  50                  55                  60
Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr Pro
  65                  70                  75                  80
Cys Gln Pro Gly Gln Arg Val Glu Val
                  85
```

```
<210> 192
<211> 299
<212> PRT
<213> mouse

<220>


<400> 192
```
```
Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp
  1               5                  10                  15
Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His
              20                  25                  30
Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr
          35                  40                  45
Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys
  50                  55                  60
Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg
  65                  70                  75                  80
Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu
                  85                  90                  95
Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr
              100                 105                 110
Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys
          115                 120                 125
Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln
      130                 135                 140
Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln
145                 150                 155                 160
Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly
                  165                 170                 175
Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly
              180                 185                 190
Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys
          195                 200                 205
Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
      210                 215                 220
Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
225                 230                 235                 240
Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
              245                 250                 255
Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly
              260                 265                 270
Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
      275                 280                 285
Pro Gln His Ser Ser Ser Lys Ala Met Lys His
      290                 295
```

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1011c2PCTSEQUENCE LISTING

```
          <210> 193
          <211> 314
          <212> PRT
          <213> mouse

          <220>
                <400> 193
Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn Ile Asp
1               5                   10                  15
Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His Val Met
            20                  25                  30
Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile
        35                  40                  45
Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr
    50                  55                  60
Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly
65              70                  75                  80
Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His
                85                  90                  95
Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys
            100                 105                 110
Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln
        115                 120                 125
Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser
    130                 135                 140
Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr
145                 150                 155                 160
Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu
                165                 170                 175
Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly
            180                 185                 190
Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu
        195                 200                 205
Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly
    210                 215                 220
Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg
225                 230                 235                 240
Cys Val Asp Thr SerGln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala
            245                 250                 255
Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly
            260                 265                 270
Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln
        275                 280                 285
Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile Leu Phe
    290                 295                 300
Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys
305                 310

          <210> 194
          <211> 109
          <212> PRT
          <213> mouse

          <400> 194
Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
```

1011c2PCTSEQUENCE LISTING

```
1                  5                      10                  15
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
            20                  25                  30
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
            35                  40                  45
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
        50                  55                  60
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile
65                      70                  75                  80
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr
                85                  90                  95
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr
            100                 105
```

```
        <210> 195
        <211> 237
        <212> PRT
        <213> mouse
```

```
        <400> 195
Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
 1                  5                      10                  15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
            20                  25                  30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
            35                  40                  45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
        50                  55                  60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
65                      70                  75                  80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
                85                  90                  95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
            100                 105                 110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
            115                 120                 125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
            130                 135                 140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145                 150                 155                 160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
                165                 170                 175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
            180                 185                 190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
            195                 200                 205
Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu
210                 215                 220
His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe
225                 230                 235
```

```
        <210> 196
        <211> 154
        <212> PRT
        <213> Human
```

1011c2PCTSEQUENCE LISTING

```
        <400> 196
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
1               5                   10                  15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
            20                  25                  30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala His Asn Ile
        35                  40                  45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
    50                  55                  60
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
65                  70                  75                  80
Lys Ala Ile Cys Arg Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu
                85                  90                  95
His Leu Thr Leu Thr Ser Tyr Ala Val Asp Ser Tyr Glu Lys Tyr Ile
            100                 105                 110
Ala Ile Gly Ile Gly Val Gly Leu Leu Leu Ser Gly Phe Leu Val Ile
        115                 120                 125
Phe Tyr Cys Tyr Ile Arg Lys Arg Cys Leu Lys Leu Lys Ser Pro Tyr
    130                 135                 140
Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
145             150
```

```
        <210> 197
        <211> 171
        <212> PRT
        <213> Rat
```

```
        <400> 197
Met Ala Arg Pro Ala Pro Trp Trp Trp Leu Arg Pro Leu Ala Ala Leu
1               5                   10                  15
Ala Leu Ala Leu Ala Leu Val Arg Val Pro Ser Ala Arg Ala Gly Gln
            20                  25                  30
Met Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr Glu
        35                  40                  45
Glu Glu Leu Ala Arg Tyr Ser Gly Glu Glu Glu Asp Gln Pro Ile Tyr
    50                  55                  60
Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu Phe
65                  70                  75                  80
Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Ala Gly Lys Asp Ser Ser
                85                  90                  95
Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His Asp
                100                 105                 110
Ile Ser Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Asp Ile Phe
        115                 120                 125
Ser Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala Arg
    130                 135                 140
Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro Glu
145             150                 155                 160
Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe
                165                 170
```

```
        <210> 198
        <211> 1399
        <212> DNA
```

1011c2PCTSEQUENCE LISTING

&lt;213&gt; Mouse

&lt;400&gt; 198
```
ggcaaagact tcggcacgag asaacagcaa agcagagctg gctgcagcca ttcactggcc
          60
tcgggcgggc gtgccacaga ggcagttgaa gtgaaagtga aagagaaacg ataagagaac
         120
ggagaccaca ggtgctaagt gagggtgctc acagaacccc ctcttcagcc agagatcact
         180
agcaggggaa ctgtggagaa ggcagccagc aaggaagagc ctgagagtag cctccatggg
         240
cttggagccc agctggtatc tgctgctctg tttggctgtc tctggggcag cagggactga
         300
ccctcccaca gcgcccacca cagcagaaag acagcggcag cccacggaca tcatcttaga
         360
ctgcttcttg gtgacagaag acaggcaccg cggggctttt gccagcagtg gggacaggga
         420
gagggccttg cttgtgctga agcaggtacc agtgctggat gatggctccc tggaaggcat
         480
cacagatttc caggggagca ctgagaccaa acaggattca cctgttatct ttgaggcctc
         540
agtggacttg gtacagattc cccaggcaga ggcgttgctc catgctgact gcagcgggaa
         600
ggcagtgacc tgcgagatct ccaagtattt cctccaggcc agacaagagg ccacttttga
         660
gaaagcacat tggttcatca gcaacatgca ggtttctaga ggtggcccca gtgtctccat
         720
ggtgatgaag actctaagag atgctgaagt tggagctgtc cggcacccta cactgaacct
         780
acctctgagt gcccagggca cagtgaagac tcaagtggag ttccaggtga catcagagac
         840
ccaaaccctg aaccacctgc tggggtcctc tgtctccctg cactgcagtt tctccatggc
         900
accagacctg gacctcactg gcgtggagtg gcggctgcag cataaaggca gcggccagct
         960
ggtgtacagc tggaagacag ggcaggggca ggccaagcgc aagggcgcta cactggagcc
        1020
tgaggagcta ctcagggctg gaaacgcctc tctcacctta cccaacctca ctctaaagga
        1080
tgaggggacc tacatctgcc agatctccac ctctctgtat caagctcaac agatcatgcc
        1140
acttaacatc ctggctcccc ccaaagtaca actgcacttg gcaaacaagg atcctctgcc
        1200
ttccctcgtc tgcagcattg ccggctacta tcctctggat gtgggagtga cgtggattcg
        1260
agaggagctg ggtggaattc agcccaagt ctctggtgcc tccttctcca gcctcaggca
        1320
gagcacgatg ggaacctaca gcatttcttc cacggtgatg gctgacccag gccccacagg
        1380
tgccacttat acctgccaa
   1399
```

&lt;210&gt; 199
&lt;211&gt; 469
&lt;212&gt; DNA

1011c2PCTSEQUENCE LISTING
<213> Rat

<400> 199
ggggcgctgg ccagtcatgg cggagccttg ggctgggcag tttctgcaag ctttgcccgc
60
cacggtgctc ggagcgctgg gcaccctggg cagcgagttt ctgcgggagt gggagacaca
120
agatatgcga gtgactctct tcaagcttct cctgctttgg ttggtgttaa gtctcctggg
180
catccagctg gcgtggggggt tctacgggaa cacagtgacc gggttgtatc accgtccagg
240
gaaatggcag caaatgaagc tctcaaaact cacagagaat aaaggaaggc agcaggagaa
300
gggtctccag agatatcgct gggtctgctg gctcctgtgc tgtaccttgc tgctatccag
360
accccttagg caactgcaga gggcttgggt tgggggactg gagtaccatg atgctcccag
420
ggtgagcctc cactgccctc agccttgcct ccaacagcgt caggtactg
469

<210> 200
<211> 529
<212> DNA
<213> Rat

<400> 200
aaagcttcca tcctcaacat gccactagtg acgacactct tctacgcctg cttctatcac
60
tacacggagt ccgagggggac cttcagcagt ccagtcaacc tgaagaaaac attcaagatc
120
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180
gatgtcgacg ccttgttcac cacaaagaac tggttgggtt acaccaagaa gagagcaccc
240
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caggaatatg tcaatctggt ggaagatgtg gacacaaagt tgaacttagc cactaagttc
360
aagtgccatg atgttgtcat tgatacttgc cgagacctga aggatcgtca acagttgctt
420
gcatacagga gcaaagtaga taaaggatct gctgaggaag agaaaatcga tgtcatcctc
480
agcagctcgc aaattcgatg gaagaactaa ggttcttttg ctacccaga
529

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<211> 1230
<212> DNA
<213> Rat

<400> 201
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120

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1011c2PCTSEQUENCE LISTING
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ggcgcccgcc aggctgctac cgagctgcgc gctcttccag gacctcatcc gctacgggaa
     180
gaccaagcag tccggctcgc ggcgccccgc cgtctgcagg gccttcgacg tccccaagag
     240
gtacttttct cacttctacg tcgtctcagt gttatggaat ggctccctgc tctggttcct
     300
gtctcagtct ctgttcctgg gagcgccgtt ccaagctgg ctttgggctt tgctcagaac
     360
tcttggggtc acgcagttcc aagccctggg gatggagtcc aaggcttctc ggatacaagc
     420
aggcgagctg gctctgtcta ccttcttagt gttggtgttc ctctgggtcc atagtcttcg
     480
gagactcttc gagtgcttct acgtcagcgt cttctctaac acggccattc acgtcgtgca
     540
gtactgtttc gggctggtct actatgtcct tgttggcctg accgtactga gccaagtgcc
     600
catgaatgac aagaacgtgt acgctctggg gaagaatcta ctgctacaag ctcggtggtt
     660
ccacatcttg ggaatgatga tgttcttctg gtcctctgcc catcagtata agtgccacgt
     720
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     780
cccctttgga gactggttcg agtatgtgtc ttctgctaac tacctagcag agctgatgat
     840
ctacatctcc atggctgtca ccttcgggct ccacaacgta acctggtggc tggtggtgac
     900
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     960
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    1020
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    1080
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    1140
acctcatccg ctacgggaag accaagcagt ccggctcgcg gcgccccgcc gtctgcagcc
    1200
cggggggatcc actagttcta gagcgccgcc
    1230

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        <212> DNA
        <213> Rat

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    300
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1011c2PCTSEQUENCE LISTING
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cactgttgta aagaacagcg tcacatttag cgcatctggc gtagtagcag tttttaacac
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    420
tgccttcctc gcacagtaag tgacctctcc atgacaaagg gcccccagac agcagttata
    480
aatcaatgtg ttttgggttt gtttgtttgt ttgttttgtt ttaaagaaaa acccggccat
    540
gcttggtggc acttgccttt aatagtagcg cttggtagac agaggcaagc ggttctctgt
    600
aagttcaagg ccagcctggt ctacacagtg agaccgggtc tcaaaaacaa aacaacaaaa
    660
aacaactcct attgaatcca ctacaggaag gggggcgcg gatcactgtc tgcaaactaa
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        <212> DNA
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    120
cgggtgccta cagcccccat cagcttcccc ggggagattc tgccgatttg tcacgagcca
    180
tgctcaggag gcagctcgtc tggtggcacc tgctggcttt gcttttcctc ccattttgcc
    240
tgtgtcaaga tgaatacatg gagtctccac aagctggagg actgcccca gactgcagca
    300
agtgttgcca tggagattat ggattccgtg gttaccaagg ccccctgga cccccaggtc
    360
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    420
gggccaaggg tgagaaagga gacaaaggcg acctggggcc tcgaggggaa cgggggcagc
    480
atggccccaa aggatagaag ggatacccag gggtgccacc agagctgcag attgcgttca
    540
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    600
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    660
gcgtgtattt cttcaccttc agcatgatga agcatgagga cgtggaggaa gtgtatgtgt
    720
accttatgca caatggtaac acggtgttca gcatgtacag ctatgaaaca aagggaaaat
    780
cagatacatc cagcaaccat gcagtgctga agttggccaa aggagatgaa gtctggctaa
    840
gaatgggcaa cggtgccctc catggggacc accagcgctt ctctaccttc gcaggctttc
    900
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    960
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1011c2PCTSEQUENCE LISTING
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taactgttac attggtcaca ctgctactca ttctaatggc ataccaatta tgttggatac
    1080
tttaggggct aggaagaata gaccacaagg taatattccc aga
    1123
```

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        <211> 434
        <212> DNA
        <213> Mouse

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    120
agagatgaaa tttttgctaa acttcaaccg aagcttagat gcacattagg tgacatggaa
    180
agtcctgtgt ttgcacttcc tgtactgtta aagcttgaac cccatgttga aagcctcttt
    240
acatattctt tttcttggaa ttttgaatgt tcccattgtg gacaccagta ccaaaacagg
    300
tgtgtgaaga gtctggtcac ctttaccaat attgttcctg agtggcatcc actcaatgct
    360
gcccattttg gtccatgtaa cagctgcaac agtaaatcac aaataagaaa aatggtgttg
    420
gaaagagcgt cgcc
    434
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        <211> 783
        <212> DNA
        <213> Mouse

        <400> 205
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    120
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cttaagtcag gaggaggctc aggccgtgga ccaagagctt tttaacgagt atcagttcag
    240
cgtggatcaa ctcatggagc tggccgggtt gagctgtgcc acggctattg ccaaggctta
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    420
tatctattac cccaaaagac ctaacaagcc cctcttcact gggctagtga ctcagtgtca
    480
gaaaatggac attcctttcc ttggtgaaat gccccagag gatgggatgt agagaaggga
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1011c2PCTSEQUENCE LISTING

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      720
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      780
aaa
      783


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         <211> 480
         <212> DNA
         <213> Mouse

         <400> 206
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ggcacgagtt aaggttttca gactttattt catggtattt gacattgaca catactgagt
      120
tagtaacaag ataccatgca gctccctcta gcctcggatc accgaagcag gaagaaggtc
      180
agactgcccc catcccagat ttgcttagtt tgtctcccaa tgtgctggac tttaaagaca
      240
gggaatggag aagcagatgg atgcttcagt ttcagtcatt tttggctcta tagtgatctc
      300
tgccttcctg tacctgtcct tggctggacc ctgggcagta actgtcactc agatgaggac
      360
gatcatcatt acaatggacc aactgaggga tgccctcata ttagaccaat taaaagttgc
      420
tgtgagttaa accaggaatg accgcacttc cacatcagaa atcaaacaaa atcaatggtt
      480


         <210> 207
         <211> 501
         <212> DNA
         <213> Mouse

         <400> 207
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      120
cagcatcgtt cttatatgcg actaacagaa aaggaagatg aatcattacc aatagatata
      180
gttcttcaga cacttctggc ctttgcagtt acctgttatg gcatagttca tatcgcaggg
      240
gagttcaaag acatggatgc cacttcagaa ttaaagaata agacatttga taccttaagg
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      360
gcaacaaatt cttcaaacct agatgcattg tcctctaata catcgttgaa gttacgaaag
      420
tttgactcac tgcgccgtta agcttttac aaattaaata acaggacaga cacagaattg
      480
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1011c2PCTSEQUENCE LISTING
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        <212> DNA
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    120
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    240
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    300
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    360
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    420
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    480

        <210> 209
        <211> 962
        <212> DNA
        <213> Mouse

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    120
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    180
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    240
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    300
ggacggccag tgcaccagca tcagccctct gaaggagctg gtgtgcgcgg gcgagtgctt
    360
gcccctgccg gtgcttccca actggatcgg aggaggctac ggaacaaagt actggagccg
    420
gaggagctct caggagtggc ggtgtgtcaa cgacaagacg cgcacccaga ggatccagct
    480
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    600
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1011c2PCTSEQUENCE LISTING

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aatgagtggt ttgcagtgaa agccaggcat cctgtagttt ccatcccctc ccccatccca
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gtcatttctt taaaagcacc tgatgctgca ttctgttaca gtttaaaaaa aaaaaaaaaa
960
aa
962

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        <211> 778
        <212> DNA
        <213> Mouse

        <400> 210
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ggtggggaac acagcgccgg ggctcggaga ccatggcggg cgctgcggtg aagtacttaa
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240
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420
attaccccaa aagacctaac aagcccctct tcactgggct agtgactcag tgtcagaaaa
480
tggacattcc tttccttggt gaaatgcccc cagaggatgg gatgtagaga agggaaaccc
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660
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720
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778

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        <212> DNA
        <213> Mouse

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caggctgggc cacaggaagc tgctgactgg ccacttgaca ccctccccct aaagctaatg
120

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1011c2PCTSEQUENCE LISTING

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tctgtgacta taggggaggtt agcactttt  ctaattggaa  ttcttctctg  tcctgtggcc
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    240
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    360
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   360
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1011c2PCTSEQUENCE LISTING

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        <211> 2728
        <212> DNA
        <213> Mouse


        <400> 213
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    120
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    180
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    960
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    1020
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    1080
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    1140
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    1200
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    1260
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    1320

1011c2PCTSEQUENCE LISTING

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    1440
tttttttaag aaccagattg cagaccgttt gtaaagagcc tctttattta acatttgtat
    1500
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    1560
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    1620
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    1680
ggggaaaaaa gtaaattaac agcataagca ttgtgggtga agagttttat tcagatcttt
    1740
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    1800
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    1920
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    1980
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    2040
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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING
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        1740
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        1800
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        1860
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        1920
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        2046


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        493


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        <212> DNA
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        180
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        240

1011c2PCTSEQUENCE LISTING
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         <211> 1107
         <212> DNA
         <213> Rat


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1011c2PCTSEQUENCE LISTING

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        <212> DNA
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        <212> DNA
        <213> Rat

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1011c2PCTSEQUENCE LISTING

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420
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1860
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1011c2PCTSEQUENCE LISTING

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    2040
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    2100
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    180
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    180
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1011c2PCTSEQUENCE LISTING

433

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  530


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        <211> 550
        <212> DNA
        <213> Mouse

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1011c2PCTSEQUENCE LISTING
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1011c2PCTSEQUENCE LISTING
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     1560
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     1620
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     1752


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     300
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     360
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1011c2PCTSEQUENCE LISTING
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       900
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1011c2PCTSEQUENCE LISTING
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aaaaa
   2165
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        <212> DNA
        <213> Mouse

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   120
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   180
gaacgcaaga gtccttatgt cgccatatgc tgtatagtga tggccttcag catcctcttc
   240
atacagtagc tttggaaact accagcatgt gcttgctatc agactgtaaa caaggacttg
   300
cctccagaaa ataatgggaa gaatggttaa gccatttgtc tctgaacatg gaatgagata
   360
aacttcaaga tgctgttctc tatttttatg ctattggacc aatgagctga atgaataatt
   420
aagatgtaac agttcaatac acaggaatgt gattgtatcc atcaacctca gttctctcac
   480
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   600
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   720
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   780
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   1200
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1011c2PCTSEQUENCE LISTING
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gctctttta aaagtttgaa aaaaaaaa
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    360
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    420
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    960
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    1020
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    1140

1011c2PCTSEQUENCE LISTING

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      1800
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      1860
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        <213> Rat

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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&lt;400&gt; 230

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1011c2PCTSEQUENCE LISTING

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     840
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1011c2PCTSEQUENCE LISTING
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atcactcaaa aggggtttcc tagaaagaaa gacaagtgac ttaaaaaatc tgccagtggg
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ttcttgaagt catcgaacct a
      861
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1011c2PCTSEQUENCE LISTING

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<211> 445
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<213> Mouse

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       120
ggagcaagtg cgtgagcgga cgtgggcctg gcagctgttg caggagataa aggctctctt
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cgggaatact gaggtgcgtc tagctctcac ggacgagccc ctgaaaattt caccataggt
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       300
cttacctgat gccctttctc ctcaatcaga gtggatccct tctctactac ttgactttgg
       360
catcaacaga tctgacgtta gctgtgccca tctgcaactc tctggccatc gtctttacac
       420
tgattgttgg gaaggtcctt ggaga
       445


<210> 234
<211> 565
<212> DNA
<213> Human

<400> 234
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tctcgctggt tctgtctacc tggcctggat cctgttcttc gtgctctatg atttctgcat
       180
tgtttgtatc accacctatg ctatcaacgt gagcctgatg tggctcagtt ccggaaggt
       240
ccaagaaccc cagggcaagg ctaagaggca ctgagccctc aacccaagcc aggctgacct
       300
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       360
ctagatgtgg ggcttctaga ttaccccctc ctcctgccat acccgcacat gacaatggac
       420
caaatgtgcc acacgctcgc tcttttttac acccagtgcc tctgactctg tccccatggg
       480
ctggtctcca aagctctttc cattgcccag ggagggaagg ttctgagcaa taaagtttct
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tagatcaatc aaaaaaaaaa aaaaa
       565


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<211> 476
<212> DNA
<213> Human
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1011c2PCTSEQUENCE LISTING

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cctatctatc attaactcca tggcacaaag ttatgccaaa cgaatccagc agcggttgaa
240
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300
ggttctgcct taaattggga ggactccaag ccgggaagga aaattccctt ttccaacctg
360
tatcaatttt tacaactttt ttcctgaaag cagtttagtc catactttgc actgacatac
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476

<210> 236
<211> 607
<212> DNA
<213> Human

<400> 236
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180
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240
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300
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360
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420
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480
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cactctg
607

<210> 237
<211> 513
<212> DNA
<213> Mouse

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1011c2PCTSEQUENCE LISTING
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    180
atcactccct tcaaagcctt tcttcctttta tatcttctga ctgagctctc cctgattgac
    240
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    300
gtactgtggt ccatgtactt actaatatgt tgctttgtaa ttattttcta gcactctgtg
    360
ttacagtttc atatttgtat ttatttccaa aattaaattg taagctcctt gagggcagga
    420
ataataactt ttacatttgt atctctgcac ccccgagtgc ctagtatagt gctgagcaca
    480
tagtaggcgt ttaataaatg cttgttgaag tat
    513


        <210> 238
        <211> 944
        <212> DNA
        <213> Rat

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    180
aggtcaaagt gctgctggaa aagtccacta ggaaaagact acgtgatact cttacaaatg
    240
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    300
cagaatttga taatgaaaag ccagctgctg tggttgctcc tcttacaaca gggtacactg
    360
tgaaaatcag taattatgga tgggatcagt cagataagtt tgtgaaaatc tacattactt
    420
taactggagt tcatcaggtt cctgctgaga atgtgcaagt acacttcaca gagaggtcat
    480
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    540
tgaaacctat ctctgtggaa agcagttcaa aaaagtcaa gactgataca gttattatcc
    600
tatgtagaaa gaaagcagaa aacacacgat gggactactt aactcaggtg gaaaaagaat
    660
gcaaagagaa agaaaagcct tcctacgaca ctgaggcaga tcctagtgag ggattaatga
    720
atgttctaaa gaaaatttat gaagatggag atgatgacat gaagcgaacc attaataaag
    780
cgtgggtgga atcccgagag aagcaagcca gggaagacac agaattctga ggctttaaaa
    840
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    944

1011c2PCTSEQUENCE LISTING

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       <212> DNA
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       120
   ggcggattca gcccgaggag ctgtggcttt accggaaccc gtacgtggag cggaatact
       180
   tccccaccgg ccccatgttt gtcattgcct ttctcacccc actgtccctg atcttcttcg
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   ccaagtttct gaggaaagct gacgccaccg acagcaagca agcctgcctc gctgccagcc
       300
   ttgccctagc tctgaatggt gtctttacca acatcataaa actgatagtg ggcaggccac
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   gcccagattt cttctaccga tgcttc
       386


       <210> 240
       <211> 228
       <212> DNA
       <213> Rat


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   cgcgctctcc ctttacgtct tcaccatcgc cactgatcct ttgcgagtca tcttcctcat
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   cgccggtgcc ttcttctggt tggtgtctct gctgctttcg tctgttttct ggttcctagt
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   gagagtcatc actgacaaca gagatggacc agtacagaat tacctgct
       228


       <210> 241
       <211> 452
       <212> DNA
       <213> Human


       <400> 241
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   ttgttaggaa aatgtaggct accagtagaa aatgacattc tctattaata agatctgagg
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   tgcgacacac ataattgtcc caatttttaa gattgatggg gagcatgaag cattttttta
       180
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       240
   ttttagggct ttctgggaat tgtcttgaca gagaacctca gctggacaaa gcagccttga
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   tctgagtgag ctaactgaca caatgaaact gtcaggcatg tttctgctcc tctctctggc
       360
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1011c2PCTSEQUENCE LISTING

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452

<210> 242
<211> 1311
<212> DNA
<213> Mouse

<400> 242
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120
ttttccccac ctgctgccct cacctgagcc cagcccagag ggcagctacg tgggccagca
180
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420
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1260
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1311

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1011c2PCTSEQUENCE LISTING

              &lt;210&gt; 243
              &lt;211&gt; 399
              &lt;212&gt; DNA
              &lt;213&gt; Mouse

              &lt;400&gt; 243

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aagggtcctg aagtcagttg ttgcatcaaa tacttcattt ttggcttcaa tgtcatattt
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  240
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  300
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  360
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  399
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              &lt;210&gt; 244
              &lt;211&gt; 1421
              &lt;212&gt; DNA
              &lt;213&gt; Mouse

              &lt;220&gt;
              &lt;221&gt; unsure
              &lt;222&gt; (1370)...(1370)

              &lt;221&gt; unsure
              &lt;222&gt; (1395)...(1395)

              &lt;400&gt; 244

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  180
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  360
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  420
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  480
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  600
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1011c2PCTSEQUENCE LISTING

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    720
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    780
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    840
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    900
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    1080
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    1140
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    1200
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    1320
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    1380
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        <211> 461
        <212> DNA
        <213> Mouse

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    360
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caagttctcc tttgcttctt gccctcccag atagaccctt g
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        <212> DNA

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1011c2PCTSEQUENCE LISTING
<213> Mouse

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    360
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    420
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    480
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    540
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    600
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    660
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    720
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    960
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    1260
aataaatacc aaacagtgaa
    1280


        <210> 247
        <211> 833
        <212> DNA
        <213> Rat

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1011c2PCTSEQUENCE LISTING

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     300
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     420
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     480
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     540
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     600
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     660
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     720
tcctccccat cactataaca cacaaccgcc gagctgtgca gagtgttcag ggccatccag
     780
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         <211> 1308
         <212> DNA
         <213> Rat

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     360
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     420
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     480
gcactcatca cgcgccagaa gcacaaggcc acagcctact acccgtcctc tttccccgaa
     540
aagaagtatg tggaccagag agaccgggct ggggggcccc atgccttcag cgaggtccct
     600
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1011c2PCTSEQUENCE LISTING
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     780
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1011c2PCTSEQUENCE LISTING

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          <211> 568
          <212> DNA
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          <212> DNA
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          <400> 254

1011c2PCTSEQUENCE LISTING
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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING

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     <213> Mouse

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agcgtagtgt gtgagtgcca cccgggatgg accggtccgc tatgtgatca ggaagctcgg
     120

1011c2PCTSEQUENCE LISTING

gacccctgcc ttggtcacag ctgcaggcac gggacatgca tggcgactgg ggactcctac
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gtgtgcaagt gtgccgaggg ctacggaggg gctttgtgtg accagaagaa tgactctgcc
     240
agtgcctgct cagccttcaa gtgccaccat gggcagtgtc acatctcaga tcgaggggag
     300
ccctattgcc tatgccagcc tggcttcagt ggccatcact gtgagcaaga gaatccatgt
     360
atggggagga tagtccgtga agccatccgc cgccagaaag actacgcctc ttgtgccacg
     420
gcgtccaagg tgcccatcat ggaatgccgc gggggctgcg ggaccacgtg ctgccagccg
     480
attcgaagca agcggcggaa atatgtcttc cagtgcacgg acggctcctc attcgtggaa
     540
gaggtggaga gacacttgga atgtggctgc cgcgcgtgtt cctgagcccc ctctgccacc
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cacccatcct ccgcctttcg gaccccagct cattgggctg ggaacagcca catggaacct
     660
ctttgagatt cagaacgaag gagagaaatc tggagagcaa gaggcaaaag agagaatatt
     720
aagtatattg taaaataacc aaaaatagaa cttatttta ttatggaaag tgactatttt
     780
catcttttat tatataaata tatcacaccg tctgagtata tggactatac agtgagttat
     840
ttttaccaag ttttgttttg tgttgtgtat ttgttgtgtt tttataaaca gctgtttata
     900
aaattttaag acaaagaaaa aacactaata aaaatgtttt aaacac
     946


     <210> 259
     <211> 1018
     <212> DNA
     <213> Human

     <400> 259
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agccgggctt ccagctgggg cctaacaacc gctcctgtgt tgatgtgaac gagtgtgaca
     120
tggggccccc atgcgagcag cgctgcttca actcctatgg gaccttcctg tgtcgctgcc
     180
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     240
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     300
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     360
ctggtgcgca ccagtgctcc gaggcccaaa cctgtgtcaa cttccatggg ggctaccgct
     420
gcgtggacac caaccgctgc gtggagccct acatccaggt ctctgagaac cgctgtctct
     480
gcccggcctc caaccctcta tgtcgagagc agccttcatc cattgtgcac cgctacatga
     540
ccatcacctc ggagcggagc gtgcccgctg acgtgttcca gatccaggcg acctccgtct
     600

1011c2PCTSEQUENCE LISTING

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accccggtgc ctacaatgcc tttcagatcc gtgctggaaa ctcgcagggg gacttttaca
    660
ttaggcaaat caacaacgtc agcgccatgc tggtcctcgc ccggccggtg acgggccccc
    720
gggagtacgt gctggacctg gagatggtca ccatgaattc cctcatgagc taccgggcca
    780
gctctgtact gaggctcacc gtctttgtag gggcctacac cttctgagga gcaggaggga
    840
gccaccctcc ctgcagctac cctagctgag gagcctgttg tgaggggcag aatgagaaag
    900
gcccaggggc ccccattgac aggagctggg agctctgcac cacgagcttc agtcaccccg
    960
agaggagagg aggtaacgag gagggcggac tccaggcccc ggcccagaga tttggact
    1018
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        <210> 260
        <211> 2800
        <212> DNA
        <213> Mouse

        <400> 260

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    60
gagacagctg cattactgtg ggcaacacta ccacacacgt gatgaagaac ctccttccag
    120
aaacgacata ccggatcaga attcaggcta tcaatgaaat tggagttgga ccatttagtc
    180
agttcattaa agcaaaaact cggccattac cgccttcgcc tcctaggctt gagtgtgctg
    240
cgtctggtcc tcagagcctg aagctcaagt ggggagacag taactccaag acacatgctg
    300
ctggtgacat ggtgtacaca ctacagctgg aagacaggaa caagaggttt atctcaatct
    360
accgaggacc cagccacacc tacaaggtcc agagactgac agagtttacc tgctactcct
    420
tcaggatcca ggcaatgagc gaggcagggg aggggcctta ctcagaaacc tacaccttca
    480
gcacaaccaa aagcgtgcct cccaccctca agcacctcg agtgacgcag ttagaaggga
    540
attcctgtga aatcttctgg gagacggtac caccgatgag aggcgaccct gtgagctacg
    600
ttctacaggt gctggttgga agagactctg agtacaagca ggtgtacaag ggagaagaag
    660
ccacattcca aatctcaggc ctccagagca acacagatta caggttccgc gtgtgtgcct
    720
gccgccgctg tgtggacacg tctcaggagc tcagtggcgc gttcagcccc tctgcggctt
    780
tcatgttaca acagcgtgag gttatgctta caggggacct gggaggcatg aagaggcca
    840
agatgaaggg catgatgccc accgacgaac agtttgctgc actcatcgtg cttggcttcg
    900
cgaccctgtc cattttgttt gcctttatat tacagtactt cttaatgaag taaatccagc
    960
aggccagtgg tatgctcgga acgccacacg ttttaataca catttactca gagcctcccc
    1020
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1011c2PCTSEQUENCE LISTING

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ttttttacgct gtttcgttct ttgatttata cgcttctctt gttttacaca tttagctagg
    1080
ggaaagagtt tggctgcacc tatttgagat gcaaaactag gaagaggtta aactggattt
    1140
tttttttaaac aataataaat aaaggaataa agaagagaag gaagcggcgg gcaagctcca
    1200
gacaccgaga gccagtgtgc ccaacgagct tgccttgtcg ggcttccccg tgtgcttctg
    1260
gtctgttccc actgatgtct ttcgcaagcc tttgatcatc ttgtgtgtta cagttcagta
    1320
atttatattc acagtcattt cttgatcatc tatacctgtt aacagaatca cagtgtatgt
    1380
agttcagggc tgggattccg gtgttgtcag agtattgcca catgagaata ttcagtgtgc
    1440
cttcggagga ggccacctcg accatcctta cgtcactcag ttacgtaact gtgttagctc
    1500
atctaagtca aagtgtgtac tttaatctaa aatgttttat tactctgtat cccttatgat
    1560
tttaacacta tgagttgcct gtctaagaag tcacataacc aaatgcgcct ataaatgata
    1620
gagcattgta gattttcaca tcggtccata gcagtaactt taagagggca ttgtgcaata
    1680
gttagttgtt tcttgttcgg ctactttaaa agctgcttta acttgtctgt ctgtctttgt
    1740
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    1800
tatgtgacga gagctcatgg cagttgtgaa ctgtctcctt acatgttggc ccatcatatt
    1860
tgaaagactt gcctttggct attctttggg gtgtcagtga cgtgaatgaa gttgaatacc
    1920
atatttcagt gcccatgata ctaatgtagc agtagataga aatcttactg ataaagccca
    1980
ccacaaggga accatttaca tttgtcctgt ttctgggggc ttcatctggc cgcatggaga
    2040
gagggagtgg aaactggctg tgagcatgag atgtttgggg gccaaagagc ctactagatt
    2100
ctctccctgg gtctgtcact aatttgcttt gtgacctctc tgtgcctgtt ttcccatgca
    2160
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    2220
cggtgctatg taagtgcgga gaatcactct cacggattca cttagagtca tgaggtaatg
    2280
agttctaacc caaagtcatt ggatccctca accaagtcca caatgttcaa gtacctcagg
    2340
gacacttaag aagttggagg tgcaactgta ttccaaaagg gtgcgacaga cacagccgat
    2400
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    2460
ttgtgcttgg tctatgttgt ctatgatgca gtaagtaccc tgtactagct tatactattc
    2520
ccataccaaa gtcatgggga aaccaacatt attttgtttt gggtttattt atactctatt
    2580
ctgcatacag tactttaaat gccaatgaca gtgcaatctt tatttattgt aatgttaaat
    2640
gtacttatta ctaatgtgcc ctcctagcat gttatatttt gtgtgtttta tacttttgt
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1011c2PCTSEQUENCE LISTING
      2700
aattttaggt cagtttagtt ccttggcaac atctgtagta ttagccttct gacatctttc
      2760
ttgtgttttt aaagataaga gcatctaact cattaaatgc
      2800

        <210> 261
        <211> 1335
        <212> DNA
        <213> Mouse

        <400> 261
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      60
cctgtgcctg gctctgcact tatccccctc cctctctgcc agtgataatg ggtcctgcgt
      120
ggtccttgat aacatctaca cctccgacat cttggaaatc agcactatgg ctaacgtctc
      180
tggtggggat gtaacctata cagtgacggt ccccgtgaac gattcagtca gtgccgtgat
      240
cctgaaagca gtgaaggagg acgacagccc agtgggcacc tggagtggaa catatgagaa
      300
gtgcaacgac agcagtgtct actataactt gacatcccaa agccagtcgg tcttccagac
      360
aaactggaca gttcctactt ccgaggatgt gactaaagtc aacctgcagg tcctcatcgt
      420
cgtcaatcgc acagcctcaa agtcatccgt gaaaatggaa caagtacaac cctcagcctc
      480
aacccctatt cctgagagtt ctgagaccag ccagaccata aacacgactc caactgtgaa
      540
cacagccaag actacagcca aggacacagc caacaccaca gccgtgacca gccaatac
      600
cacagccaat accacagccg tgaccacagc caagaccaca gccaaaagcc tggccatccg
      660
cactctcggc agccccctgg caggtgccct ccatatcctg cttgtttttc tcattagtaa
      720
actcctcttc taaagaaaac tggggaagca gatctccaac ctccaggtca tcctcccgag
      780
ctcatttcag gccagtgctt aaacataccc gaatgaaggt tttatgtcct cagtccgcag
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      900
cctggatctt tcagggcaca aattccgctt cttgtaaata cttagtccat ccatcctgcg
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      1020
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      1080
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      1140
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      1200
tttccactgt gcccagacca gtcggtaggt tttgaaggaa gtatatgaaa actgtgcctc
      1260
agaagccaat gacaggacac atgacttttt ttttctaagt caaataaaca atatattgaa

1011c2PCTSEQUENCE LISTING
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       <210> 262
       <211> 1816
       <212> DNA
       <213> Mouse

       <400> 262
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    catgctctgc ctgtgcctgt atgtgcccat cgccggggcg gctcagactg agttccagta
        120
    ctttgagtcc aaggggcttc ctgccgagct gaaatccatc ttcaaactca gtgtctttat
        180
    cccctctcaa gagttctcca cataccgcca atggaagcag aaaattgtgc aagcaggtga
        240
    caaggacctt gatgggcaac tggactttga agagtttgta cattacctcc aagatcatga
        300
    gaaaaaactg aggctggtgt tcaagagtct ggacaaaaag aatgatggtc gaatcgatgc
        360
    tcaggagatc atgcagtccc tgcgggacct gggtgtcaag atctcggaac agcaggcgga
        420
    gaagattctt aagagcatgg ataagaatgg cacgatgacc atcgactgga acgagtggag
        480
    ggactaccac ctcctgcacc ctgtggagaa catcccggag atcatcctgt actggaagca
        540
    ctcgacgatc ttcgatgtcg gtgagaatct gacagtccca gatgagttca cagtggagga
        600
    gaggcagacg gggatgtggt ggaggcacct ggtggcagga ggtggggcag gggcagtttc
        660
    cagaacctgc actgcccccc tggacagact gaaggtgctc atgcaggtcc atgcctcccg
        720
    cagcaacaac atgtgcatcg taggtggatt cacacagatg attcgagaag ggggagccaa
        780
    gtcactctgg cggggcaacg gcatcaatgt cctcaaaatt gcccctgagt cggccatcaa
        840
    attcatggca tatgagcaga tgaaacggct tgtcggtagt gatcaggaga cgctgaggat
        900
    ccacgaaagg cttgtggcag gctccttggc cggagccatt gcccagagta gcatctaccc
        960
    aatggaggtt ctgaagaccc gaatggccct gcggaaaaca ggacagtact ccggcatgct
        1020
    ggactgtgcc aggaggatct tggctaaaga gggtgtagct gccttctaca aaggctacat
        1080
    ccccaacatg ctggggatca tcccctatgc tggcatcgac ctagctgtct atgagacatt
        1140
    gaaaaatacc tggctccagc gctacgcagt aaacagtgca gaccccggtg tgttcgtgct
        1200
    cctggcctgt ggtactatct ccagtacttg tggccagctg ccagctacc cactagccct
        1260
    ggtcaggacc cggatgcagg cacaagcctc cattgagggc gcacctgagg taaccatgag
        1320
    cagcctcttc aaacagattc tgcggactga gggggccttt gggctctacc gggggctggc
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1011c2PCTSEQUENCE LISTING

1380
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1440
gaagatcacc ctgggcgtgc agtctcggtg acgggagggt ggtggacttg gtgagcctgg
1500
gctgcggccc agggtatgca gccacctcat tctgtgaatg tgccaacact aagctgactt
1560
acccaagctg tgaaacccag gataccatag gggacgggca gggagctggc aagctctggg
1620
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1680
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1740
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1800
ggacctcagc cacggg
1816

        <210> 263
        <211> 764
        <212> DNA
        <213> Mouse

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120
cgggcggcat ccccgggccg ccgcacgcac aggccggcgc cctccttgcc tccctgctcc
180
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gatccgctac agcgacgtga agaagctgga aatgaagcca agtacccac actgcgagga
360
gaagatggtt atcgtcacca ccaagagcat gtccaggtac cggggccagg agcactgcct
420
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480
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660
gctgtgtgtg aaaggcttcc agatgtgaga tccagctcgc ctgcgcacca gacttcatta
720
caagtggctt tttgctgggc ggttggcggg gggcggggggg acct
764

        <210> 264
        <211> 1697
        <212> DNA
        <213> Mouse

1011c2PCTSEQUENCE LISTING

<400> 264

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       120
gagtcacccg aagcccctcc gcagtcctgg acacagctgt ggctcttccg cttcttgttg
       180
aatgtagcgg gctatgccag ctttatggta cctggctacc tcctggtgca gtacttaaga
       240
cggaagaact acctggagac aggcaggggt ctctgcttcc ccctggtgaa agcctgtgtg
       300
tttggcaatg agcccaaggc tcctgatgag gttctcctgg ctccgcggac agagacagcg
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gaatccaccc cgtcttggca ggtcctgaag ctggtcttct gtgcctcggg tctccaggtg
       420
tcctatctga cttggggcat actgcaggaa agagtgatga ctggcagcta cggggccaca
       480
gccacatcac caggagagca tttcacagac tcccagtttc tggtgctgat gaaccgtgtg
       540
ctggcgctgg ttgtggcagg cctctactgt gtcctgcgca agcagccccg tcatggtgca
       600
cccatgtacc ggtactcctt tgccagtctg tcaaatgtgc ttagcagctg gtgccagtat
       660
gaagcactta agttcgtcag cttccctacc caggtgctgg cgaaggcctc caaggtgatc
       720
cctgtcatga tgatgggaaa gctggtgtcc cggcgcagct atgaacactg ggaatacctg
       780
actgccggcc tcatctccat tggagtgagc atgtttcttc tatccagtgg accagagcct
       840
agaagctctc cagccaccac actctctggc ttggtcctac tggcaggcta tattgctttc
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gacagcttca cctcaaattg gcaggatgcc ctgtttgcct ataagatgtc atcggtgcag
       960
atgatgtttg gggtcaattt attctcctgt cttttcacag taggctcact actggaacag
      1020
ggggccctac tggagggggc acgcttcatg gggcggcaca gtgagtttgc gctccatgct
      1080
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      1140
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      1200
tcctgcctcc tctatggcca tactgtcact gtggtggggg gactgggagt agctgtggtc
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      1320
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      1380
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      1500
cagagctcct cccccaatct ctgaaatctt gctggtggcc aagcaaacca gcaccagggc
      1560
tttgctcata gcacgcaccc ttgaggctac caggcaccag ctgggaagag aatttacagg
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1011c2PCTSEQUENCE LISTING
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1620
tcctgcagtt cccctagggg ccagtgagaa tggtgctgtg ccagaaggga caaaggcccc
    1680
cagcccagtt ggggccc
    1697
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        <210> 265
        <211> 159
        <212> DNA
        <213> Mouse

        <220>


        <400> 265
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    60
aaccaaagca gcggccgcgg ccggagcccc tcatcatccc caccaaggcg ggcactttca
    120
tcgcccctcc tgtctactcc aacatcaccc cttaccaga
    159
```

```
        <210> 266
        <211> 292
        <212> DNA
        <213> Mouse

        <400> 266
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    60
ctggtggcat ggactatggt atggttggtg gcaaggaggc tgggaccgag tctcgcttca
    120
aacagtggac ctcaatgatg gaagggctgc catctgtggc cacacaagaa gccaccatgc
    180
acaaaaacgg cgctatagtg gcccctggta agacccgagg aggttcacca tacaaccagt
    240
ttgatataat cccaggtgac acactgggtg gccatacggg tcctgctggt ga
    292
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```
        <210> 267
        <211> 339
        <212> DNA
        <213> Mouse

        <400> 267
ccactgacct tcccagaagg tgacagccgg cggcggatgt tgtcaaggag ccgagatagt
    60
ccagcagtgc ctcggtaccc agaagacggg ctgtctcccc ccaaaagacg gcgacattcg
    120
atgagaagtc accacagtga tctcacattt tgcgagatta tcctgatgga gatggagtcc
    180
catgatgcag cctggccttt cctagagcct gtgaaccctc gcttggtgag tggataccga
    240
cgtgtcatca agaaccctat ggatttttcc accatgcgag aacgcctgct ccgtggaggg
    300
```

1011c2PCTSEQUENCE LISTING
tacactagct cagaagagtt tgcagctgat gctctgctg
    339

        <210> 268
        <211> 153
        <212> DNA
        <213> Mouse

        <400> 268
ctgaagttct ctcatccttg tctggaagac cataatagtt actgcattaa tggagcatgt
    60
gcattccacc atgagctgaa gcaagccatt tgcagatgct ttactggtta tacgggacaa
    120
cgatgtgagc atttgaccct aacttcgtat gct
    153

        <210> 269
        <211> 153
        <212> DNA
        <213> Human

        <400> 269
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    60
gcattccacc atgagctaga gaaagccatc tgcaggtgtt ttactggtta tactggagaa
    120
aggtgtgagc acttgacttt aacttcatat gct
    153

        <210> 270
        <211> 288
        <212> DNA
        <213> Human

        <400> 270
gcggccgcgc tgctcctgct gctgctggcg ctgtacaccg cgcgtgtgga cgggtccaaa
    60
tgcaagtgct cccggaaggg acccaagatc cgctacagcg acgtgaagaa gctggaaatg
    120
aagccaaagt acccgcactg cgaggagaag atggttatca tcaccaccaa gagcgtgtcc
    180
aggtaccgag gtcaggagca ctgcctgcac cccaagctgc agagcaccaa gcgcttcatc
    240
aagtggtaca acgcctggaa cgagaagcgc agggtctacg aagaatag
    288

        <210> 271
        <211> 234
        <212> DNA
        <213> Mouse

        <400> 271
tccaagtgta agtgttcccg gaaggggccc aagatccgct acagcgacgt gaagaagctg
    60
gaaatgaagc caaagtaccc acactgcgag gagaagatgg ttatcgtcac caccaagagc

1011c2PCTSEQUENCE LISTING
        120
atgtccaggt accgggggcca ggagcactgc ctgcacccta agctgcagag caccaaacgc
        180
ttcatcaagt ggtacaatgc ctggaacgag aagcgcaggg tctacgaaga atag
        234

        <210> 272
        <211> 234
        <212> DNA
        <213> Human.
        <400> 272
tccaaatgca agtgctcccg gaagggaccc aagatccgct acagcgacgt gaagaagctg
        60
gaaatgaagc caaagtaccc gcactgcgag gagaagatgg ttatcatcac caccaagagc
        120
gtgtccaggt accgaggtca ggagcactgc ctgcacccca agctgcagag caccaagcgc
        180
ttcatcaagt ggtacaacgc ctggaacgag aagcgcaggg tctacgaaga atag
        234

        <210> 273
        <211> 645
        <212> DNA
        <213> Mouse

        <400> 273
atgctgtcgc tccgctcctt gcttccacac ctgggactgt tcctgtgcct ggctctgcac
        60
ttatccccct ccctctctgc cagtgataat gggtcctgcg tggtccttga taacatctac
        120
acctccgaca tcttggaaat cagcactatg gctaacgtct ctggtgggga tgtaacctat
        180
acagtgacgg tccccgtgaa cgattcagtc agtgccgtga tcctgaaagc agtgaaggag
        240
gacgacagcc cagtgggcac ctggagtgga acatatgaga agtgcaacga cagcagtgtc
        300
tactataact tgacatccca aagccagtcg gtcttccaga caaactggac agttcctact
        360
tccgaggatg tgactaaagt caacctgcag gtcctcatcg tcgtcaatcg cacagcctca
        420
aagtcatccg tgaaaatgga acaagtacaa ccctcagcct caaccccctat tcctgagagt
        480
tctgagacca gccagaccat aaacacgact ccaactgtga acacagccaa gactacagcc
        540
aaggacacag ccaacaccac agccgtgacc acagccaata ccacagccaa taccacagcc
        600
gtgaccacag ccaagaccac agccaaaagc ctggccatcc gcact
        645

        <210> 274.
        <211> 63
        <212> DNA
        <213> Mouse

        <400> 274

1011c2PCTSEQUENCE LISTING
gggtacagtg atggttacca agtgtgtagt aggttcggaa gcaaagtgcc tcagtttctg
            60
aac
            63


            <210> 275
            <211> 388
            <212> PRT
            <213> Mouse
            <400> 275
Met Gly Leu Glu Pro Ser Trp Tyr Leu Leu Leu Cys Leu Ala Val Ser
1               5                   10                  15
Gly Ala Ala Gly Thr Asp Pro Pro Thr Ala Pro Thr Thr Ala Glu Arg
            20                  25                  30
Gln Arg Gln Pro Thr Asp Ile Ile Leu Asp Cys Phe Leu Val Thr Glu
            35                  40                  45
Asp Arg His Arg Gly Ala Phe Ala Ser Ser Gly Asp Arg Glu Arg Ala
            50                  55                  60
Leu Leu Val Leu Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu
65                  70                  75                  80
Gly Ile Thr Asp Phe Gln Gly Ser Thr Glu Thr Lys Gln Asp Ser Pro
                85                  90                  95
Val Ile Phe Glu Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu
                100                 105                 110
Ala Leu Leu His Ala Asp Cys Ser Gly Lys Ala Val Thr Cys Glu Ile
            115                 120                 125
Ser Lys Tyr Phe Leu Gln Ala Arg Gln Glu Ala Thr Phe Glu Lys Ala
            130                 135                 140
His Trp Phe Ile Ser Asn Met Gln Val Ser Arg Gly Gly Pro Ser Val
145                 150                 155                 160
Ser Met Val Met Lys Thr Leu Arg Asp Ala Glu Val Gly Ala Val Arg
                165                 170                 175
His Pro Thr Leu Asn Leu Pro Leu Ser Ala Gln Gly Thr Val Lys Thr
                180                 185                 190
Gln Val Glu Phe Gln Val Thr Ser Glu Thr Gln Thr Leu Asn His Leu
            195                 200                 205
Leu Gly Ser Ser Val Ser Leu His Cys Ser Phe Ser Met Ala Pro Asp
            210                 215                 220
Leu Asp Leu Thr Gly Val Glu Trp Arg Leu Gln His Lys Gly Ser Gly
225                 230                 235                 240
Gln Leu Val Tyr Ser Trp Lys Thr Gly Gln Gly Gln Ala Lys Arg Lys
                245                 250                 255
Gly Ala Thr Leu Glu Pro Glu Glu Leu Leu Arg Ala Gly Asn Ala Ser
                260                 265                 270
Leu Thr Leu Pro Asn Leu Thr Leu Lys Asp Glu Gly Thr Tyr Ile Cys
            275                 280                 285
Gln Ile Ser Thr Ser Leu Tyr Gln Ala Gln Gln Ile Met Pro Leu Asn
            290                 295                 300
Ile Leu Ala Pro Pro Lys Val Gln Leu His Leu Ala Asn Lys Asp Pro
305                 310                 315                 320
Leu Pro Ser Leu Val Cys Ser Ile Ala Gly Tyr Tyr Pro Leu Asp Val
                325                 330                 335
Gly Val Thr Trp Ile Arg Glu Glu Leu Gly Gly Ile Pro Ala Gln Val
                340                 345                 350
Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Thr Met Gly Thr Tyr

1011c2PCTSEQUENCE LISTING

```
                355                    360                    365
Ser Ile Ser Ser Thr Val Met Ala Asp Pro Gly Pro Thr Gly Ala Thr
        370                    375                    380
Tyr Thr Cys Gln
385
```

```
        <210> 276
        <211> 151
        <212> PRT
        <213> Rat


        <400> 276
Met Ala Glu Pro Trp Ala Gly Gln Phe Leu Gln Ala Leu Pro Ala Thr
1               5                   10                  15
Val Leu Gly Ala Leu Gly Thr Leu Gly Ser Glu Phe Leu Arg Glu Trp
            20                  25                  30
Glu Thr Gln Asp Met Arg Val Thr Leu Phe Lys Leu Leu Leu Leu Trp
        35                  40                  45
Leu Val Leu Ser Leu Leu Gly Ile Gln Leu Ala Trp Gly Phe Tyr Gly
        50                  55                  60
Asn Thr Val Thr Gly Leu Tyr His Arg Pro Gly Lys Trp Gln Gln Met
65                  70                  75                  80
Lys Leu Ser Lys Leu Thr Glu Asn Lys Gly Arg Gln Gln Glu Lys Gly
            85                  90                  95
Leu Gln Arg Tyr Arg Trp Val Cys Trp Leu Leu Cys Cys Thr Leu Leu
            100                 105                 110
Leu Ser Arg Pro Leu Arg Gln Leu Gln Arg Ala Trp Val Gly Gly Leu
        115                 120                 125
Glu Tyr His Asp Ala Pro Arg Val Ser Leu His Cys Pro Gln Pro Cys
        130                 135                 140
Leu Gln Gln Arg Gln Val Leu
145                 150
```

```
        <210> 277
        <211> 163
        <212> PRT
        <213> Rat


        <400> 277
Met Pro Leu Val Thr Thr Leu Phe Tyr Ala Cys Phe Tyr His Tyr Thr
1               5                   10                  15
Glu Ser Glu Gly Thr Phe Ser Ser Pro Val Asn Leu Lys Lys Thr Phe
            20                  25                  30
Lys Ile Pro Asp Arg Gln Tyr Val Leu Thr Ala Leu Ala Ala Arg Ala
        35                  40                  45
Lys Leu Arg Ala Trp Asn Asp Val Asp Ala Leu Phe Thr Thr Lys Asn
        50                  55                  60
Trp Leu Gly Tyr Thr Lys Lys Arg Ala Pro Ile Gly Phe His Arg Val
65                  70                  75                  80
Val Glu Ile Leu His Lys Asn Ser Ala Pro Val Gln Ile Leu Gln Glu
            85                  90                  95
Tyr Val Asn Leu Val Glu Asp Val Asp Thr Lys Leu Asn Leu Ala Thr
            100                 105                 110
Lys Phe Lys Cys His Asp Val Val Ile Asp Thr Cys Arg Asp Leu Lys
        115                 120                 125
```

1011c2PCTSEQUENCE LISTING

Asp Arg Gln Gln Leu Leu Ala Tyr Arg Ser Lys Val Asp Lys Gly Ser
    130              135          140
Ala Glu Glu Glu Lys Ile Asp Val Ile Leu Ser Ser Ser Gln Ile Arg
145              150              155              160
Trp Lys Asn


        <210> 278
        <211> 330
        <212> PRT
        <213> Rat


        <400> 278
Met Ala Gly Trp Ala Gly Ala Glu Leu Ser Val Leu Asn Pro Leu Arg
1           5              10              15
Ala Leu Trp Leu Leu Leu Ala Ala Ala Phe Leu Leu Ala Leu Leu Leu
        20              25              30
Gln Leu Ala Pro Ala Arg Leu Leu Pro Ser Cys Ala Leu Phe Gln Asp
        35              40              45
Leu Ile Arg Tyr Gly Lys Thr Lys Gln Ser Gly Ser Arg Arg Pro Ala
    50              55              60
Val Cys Arg Ala Phe Asp Val Pro Lys Arg Tyr Phe Ser His Phe Tyr
65              70              75              80
Val Val Ser Val Leu Trp Asn Gly Ser Leu Leu Trp Phe Leu Ser Gln
            85              90              95
Ser Leu Phe Leu Gly Ala Pro Phe Pro Ser Trp Leu Trp Ala Leu Leu
        100             105             110
Arg Thr Leu Gly Val Thr Gln Phe Gln Ala Leu Gly Met Glu Ser Lys
    115             120             125
Ala Ser Arg Ile Gln Ala Gly Glu Leu Ala Leu Ser Thr Phe Leu Val
    130             135             140
Leu Val Phe Leu Trp Val His Ser Leu Arg Arg Leu Phe Glu Cys Phe
145             150             155             160
Tyr Val Ser Val Phe Ser Asn Thr Ala Ile His Val Val Gln Tyr Cys
                165             170             175
Phe Gly Leu Val Tyr Tyr Val Leu Val Gly Leu Thr Val Leu Ser Gln
            180             185             190
Val Pro Met Asn Asp Lys Asn Val Tyr Ala Leu Gly Lys Asn Leu Leu
    195             200             205
Leu Gln Ala Arg Trp Phe His Ile Leu Gly Met Met Met Phe Phe Trp
    210             215             220
Ser Ser Ala His Gln Tyr Lys Cys His Val Ile Leu Ser Asn Leu Arg
225             230             235             240
Arg Asn Lys Lys Gly Val Val Ile His Cys Gln His Arg Ile Pro Phe
            245             250             255
Gly Asp Trp Phe Glu Tyr Val Ser Ser Ala Asn Tyr Leu Ala Glu Leu
        260             265             270
Met Ile Tyr Ile Ser Met Ala Val Thr Phe Gly Leu His Asn Val Thr
    275             280             285
Trp Trp Leu Val Val Thr Tyr Val Phe Phe Ser Gln Ala Leu Ser Ala
    290             295             300
Phe Phe Asn His Arg Phe Tyr Lys Ser Thr Phe Val Ser Tyr Pro Lys
305             310             315             320
His Arg Lys Ala Phe Leu Pro Phe Leu Phe
            325             330

1011c2PCTSEQUENCE LISTING

```
        <210> 279
        <211> 61
        <212> PRT
        <213> Rat

        <400> 279
Met Glu Asn Ile Tyr Tyr Thr Asn Leu Ile Thr Ile Leu Gly Asn Lys
 1               5                  10                  15
His Ala Asn Gln Met Glu Leu Asn Leu Gln Ala Leu Ile Leu Ser Pro
            20                  25                  30
Trp Phe Ala Val Cys Ala Pro Pro Gly Phe Ala Arg Asp Gln Ala Val
        35                  40                  45
Arg Gly Leu Ala Leu Ala Gly Arg Arg Ile Thr Val Val
    50                  55                  60


        <210> 280
        <211> 105
        <212> PRT
        <213> Rat


        <400> 280
Met Leu Arg Arg Gln Leu Val Trp Trp His Leu Leu Ala Leu Leu Phe
 1               5                  10                  15
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Ser Pro Gln Ala
            20                  25                  30
Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Gly
        35                  40                  45
Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile
    50                  55                  60
Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly Ala Thr Gly His Glu
65                  70                  75                  80
Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly Asp Leu Gly Pro Arg Gly
                85                  90                  95
Glu Arg Gly Gln His Gly Pro Lys Gly
            100                 105


        <210> 281
        <211> 27
        <212> PRT
        <213> Mouse

        <400> 281
Met Leu Lys Ala Ser Leu His Ile Leu Phe Leu Gly Ile Leu Asn Val
 1               5                  10                  15
Pro Ile Val Asp Thr Ser Thr Lys Thr Gly Val
            20                  25


        <210> 282
        <211> 169
        <212> PRT
        <213> Mouse

        <400> 282
Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
```

1011c2PCTSEQUENCE LISTING

```
1                   5                        10                      15
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
                20                  25                  30
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
            35                  40                  45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
        50                  55                  60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
65                  70                  75                      80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
                85                  90                  95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
            100                 105                 110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
            115                 120                 125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
    130                 135                 140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
145                 150                 155                     160
Gly Glu Met Pro Pro Glu Asp Gly Met
                165


        <210> 283
        <211> 61
        <212> PRT
        <213> Mouse


        <400> 283
Met Glu Lys Gln Met Asp Ala Ser Val Ser Val Ile Phe Gly Ser Ile
1                   5                        10                      15
Val Ile Ser Ala Phe Leu Tyr Leu Ser Leu Ala Gly Pro Trp Ala Val
                20                  25                  30
Thr Val Thr Gln Met Arg Thr Ile Ile Ile Thr Met Asp Gln Leu Arg
            35                  40                  45
Asp Ala Leu Ile Leu Asp Gln Leu Lys Val Ala Val Ser
        50                  55                  60


        <210> 284
        <211> 131
        <212> PRT
        <213> Mouse


        <400> 284
Met Ala Pro Ser Leu Trp Lys Gly Leu Val Gly Val Gly Leu Phe Ala
1                   5                        10                      15
Leu Ala His Ala Ala Phe Ser Ala Ala Gln His Arg Ser Tyr Met Arg
                20                  25                  30
Leu Thr Glu Lys Glu Asp Glu Ser Leu Pro Ile Asp Ile Val Leu Gln
            35                  40                  45
Thr Leu Leu Ala Phe Ala Val Thr Cys Tyr Gly Ile Val His Ile Ala
        50                  55                  60
Gly Glu Phe Lys Asp Met Asp Ala Thr Ser Glu Leu Lys Asn Lys Thr
65                  70                  75                      80
Phe Asp Thr Leu Arg Asn His Pro Ser Phe Tyr Val Phe Asn His Arg
                85                  90                  95
```

1011c2PCTSEQUENCE LISTING

Gly Arg Val Leu Phe Arg Pro Ser Asp Ala Thr Asn Ser Ser Asn Leu
            100             105                 110
Asp Ala Leu Ser Ser Asn Thr Ser Leu Lys Leu Arg Lys Phe Asp Ser
            115             120                 125
Leu Arg Arg
    130

        <210> 285
        <211> 78
        <212> PRT
        <213> Mouse

        <400> 285
Gly Thr Arg Lys Pro Leu Pro Met Glu Ala His Ser Arg Arg Glu Lys
1               5               10                  15
Ala Ser Gly Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser
            20              25                  30
Val Trp Trp Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu
            35              40                  45
Leu Phe Ser Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His
    50              55                  60
Met Leu Pro Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
65                  70                  75

        <210> 286
        <211> 206
        <212> PRT
        <213> Mouse

        <400> 286
Met Leu Pro Pro Ala Ile His Leu Ser Leu Ile Pro Leu Leu Cys Ile
1               5               10                  15
Leu Met Arg Asn Cys Leu Ala Phe Lys Asn Asp Ala Thr Glu Ile Leu
            20              25                  30
Tyr Ser His Val Val Lys Pro Val Pro Ala His Pro Ser Ser Asn Ser
            35              40                  45
Thr Leu Asn Gln Ala Arg Asn Gly Gly Arg His Phe Ser Ser Thr Gly
    50              55                  60
Leu Asp Arg Asn Ser Arg Val Gln Val Gly Cys Arg Glu Leu Arg Ser
65                  70                  75                  80
Thr Lys Tyr Ile Ser Asp Gly Gln Cys Thr Ser Ile Ser Pro Leu Lys
            85                  90                  95
Glu Leu Val Cys Ala Gly Glu Cys Leu Pro Leu Pro Val Leu Pro Asn
            100             105                 110
Trp Ile Gly Gly Gly Tyr Gly Thr Lys Tyr Trp Ser Arg Arg Ser Ser
            115             120                 125
Gln Glu Trp Arg Cys Val Asn Asp Lys Thr Arg Thr Gln Arg Ile Gln
    130             135                 140
Leu Gln Cys Gln Asp Gly Ser Thr Arg Thr Tyr Lys Ile Thr Val Val
145             150                 155                 160
Thr Ala Cys Lys Cys Lys Arg Tyr Thr Arg Gln His Asn Glu Ser Ser
                165                 170                 175
His Asn Phe Glu Ser Val Ser Pro Ala Lys Pro Ala Gln His His Arg
            180             185                 190
Glu Arg Lys Arg Ala Ser Lys Ser Ser Lys His Ser Leu Ser

1011c2PCTSEQUENCE LISTING
195                          200                          205

```
<210> 287
<211> 169
<212> PRT
<213> Mouse

<400> 287
Met Ser Gly Leu Arg Thr Leu Leu Gly Leu Gly Leu Leu Val Ala Gly
1               5                   10                  15
Ser Arg Leu Pro Arg Val Ile Ser Gln Gln Ser Val Cys Arg Ala Arg
            20                  25                  30
Pro Ile Trp Trp Gly Thr Gln Arg Arg Gly Ser Glu Thr Met Ala Gly
        35                  40                  45
Ala Ala Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln
    50                  55                  60
Glu Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
65                  70                  75                  80
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro Thr
                85                  90                  95
Ser Met Ser Lys Ser Pro Pro Thr Val Leu Val Ile Cys Gly Pro Gly
            100                 105                 110
Asn Asn Gly Gly Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe
            115                 120                 125
Gly Tyr Gln Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu
            130                 135                 140
Phe Thr Gly Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu
145                 150                 155                 160
Gly Glu Met Pro Pro Glu Asp Gly Met
                165

<210> 288
<211> 114
<212> PRT
<213> Mouse

<400> 288
Met Ser Val Thr Ile Gly Arg Leu Ala Leu Phe Leu Ile Gly Ile Leu
1               5                   10                  15
Leu Cys Pro Val Ala Pro Ser Leu Thr Arg Ser Trp Pro Gly Pro Asp
            20                  25                  30
Thr Cys Ser Leu Phe Leu Gln His Ser Leu Ser Leu Ser Leu Arg Leu
        35                  40                  45
Gly Gln Ser Leu Glu Gly Gly Leu Ser Val Cys Phe His Val Cys Ile
    50                  55                  60
His Ala Cys Glu Cys Val Ala Cys Cys Arg Val Leu Trp Asp Pro Lys
65                  70                  75                  80
Pro Arg Gly Ser Ser Leu Cys Arg Trp Val Leu Gly Ser Ile Thr Cys
                85                  90                  95
Leu Phe Met Tyr Glu Val Gly Gly Trp Thr Gln Gly Gly Leu Ile Val
            100                 105                 110
Ser Leu
```

`<210> 289`

1011c2PCTSEQUENCE LISTING

&lt;211&gt; 46
&lt;212&gt; PRT
&lt;213&gt; Mouse

&lt;400&gt; 289

| Met<br>1 | His | Tyr | Pro | Cys<br>5 | Leu | Ala | Cys | Leu | Phe<br>10 | Val | Asn | Val | His | Trp<br>15 | Cys |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Phe | Ala | Trp | Met<br>20 | Cys | Ile | Leu | Val | Lys<br>25 | Met | Ser | Glu | Leu | Leu<br>30 | Glu | Leu |
| Glu | Leu | Glu<br>35 | Thr | Met | Val | Ser | Cys<br>40 | Leu | Val | Asp | Val | Gly<br>45 | Asn | | |

&lt;210&gt; 290
&lt;211&gt; 199
&lt;212&gt; PRT
&lt;213&gt; Mouse

&lt;400&gt; 290

| Met<br>1 | Val | Leu | Pro | Thr<br>5 | Val | Leu | Ile | Leu | Leu<br>10 | Leu | Ser | Trp | Ala | Ala<br>15 | Gly |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Leu | Gly | Gly | Glu<br>20 | Thr | Arg | Pro | Arg | Ala<br>25 | Ala | Thr | Glu | Arg | Arg<br>30 | Ser | Val |
| Gly | Pro | Ser<br>35 | Ala | Arg | Arg | Gly | Ala<br>40 | Gly | Pro | Arg | Val | Ser<br>45 | Gly | Leu | Leu |
| Gly | Phe<br>50 | Cys | Gln | Leu | Ser | Gln<br>55 | Leu | Ala | Ser | Ala | Asp<br>60 | Pro | Glu | Arg | Arg |
| Ser<br>65 | Pro | Arg | Ala | Ile | Val<br>70 | Pro | Arg | Ala | Pro | Arg<br>75 | Pro | Arg | Ser | Arg | Arg<br>80 |
| Arg | Pro | Cys | Leu | Pro<br>85 | Gly | Phe | Ser | Arg | Arg<br>90 | Phe | Pro | Arg | Glu | Arg<br>95 | Arg |
| Ser | Pro | Gly | Gln<br>100 | Pro | Pro | Ser | Arg | Thr<br>105 | Pro | Gln | Pro | Pro | Gln<br>110 | Pro | Cys |
| Arg | Gly | Pro<br>115 | Ser | Pro | Gly | Thr | Ala<br>120 | Gln | Thr | Arg | Ser | Asn<br>125 | Leu | Arg | Gly |
| Trp | Gln<br>130 | Arg | Gly | Gly | Ser | Ile<br>135 | Val | Leu | Gln | Ala | Ser<br>140 | Glu | Arg | Thr | Arg |
| Ala<br>145 | Gly | Cys | Arg | Thr | Pro<br>150 | Val | Cys | Val | Ser | His<br>155 | Pro | Ser | Ala | Phe | Pro<br>160 |
| Pro | Pro | Arg | Ala | Leu<br>165 | Phe | Gly | Val | Phe | Val<br>170 | Ala | Ser | Ala | Pro | Glu<br>175 | Val |
| Val | Cys | Val | Cys<br>180 | Val | Ser | Val | Val | Leu<br>185 | Ser | Val | Cys | Leu | Leu<br>190 | Ser | Pro |
| Arg | Gly | Lys<br>195 | Thr | Leu | Val | Asp | | | | | | | | | |

&lt;210&gt; 291
&lt;211&gt; 568
&lt;212&gt; PRT
&lt;213&gt; Rat

&lt;400&gt; 291

| Met<br>1 | Glu | Leu | Leu | Tyr<br>5 | Trp | Cys | Leu | Leu | Cys<br>10 | Leu | Leu | Leu | Pro | Leu<br>15 | Thr |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Ser | Arg | Thr | Gln<br>20 | Lys | Leu | Pro | Thr | Arg<br>25 | Asp | Glu | Glu | Leu | Phe<br>30 | Gln | Met |

1011c2PCTSEQUENCE LISTING

Gln Ile Arg Asp Lys Ala Leu Phe His Asp Ser Ser Val Ile Pro Asp
        35                      40                      45
Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Asp Thr Pro Arg Arg Tyr
    50                      55                      60
Phe Phe Met Val Glu Glu Asp Asn Thr Pro Leu Ser Val Thr Val Thr
65                      70                      75                      80
Pro Cys Asp Ala Pro Leu Glu Trp Lys Leu Ser Leu Gln Glu Leu Pro
                85                      90                      95
Glu Glu Ser Ser Ala Asp Gly Ser Gly Asp Pro Glu Pro Leu Asp Gln
            100                     105                     110
Gln Lys Gln Gln Met Thr Asp Val Glu Gly Thr Glu Leu Phe Ser Tyr
    115                     120                     125
Lys Gly Asn Asp Val Glu Tyr Phe Leu Ser Ser Ser Ser Pro Ser Gly
    130                     135                     140
Leu Tyr Gln Leu Glu Leu Leu Ser Thr Glu Lys Asp Thr His Phe Lys
145                     150                     155                     160
Val Tyr Ala Thr Thr Thr Pro Glu Ser Asp Gln Pro Tyr Pro Asp Leu
                165                     170                     175
Pro Tyr Asp Pro Arg Val Asp Val Thr Ser Ile Gly Arg Thr Thr Val
            180                     185                     190
Thr Leu Ala Trp Lys Gln Ser Pro Thr Ala Ser Met Leu Lys Gln Pro
        195                     200                     205
Ile Glu Tyr Cys Val Val Ile Asn Lys Glu His Asn Phe Lys Ser Leu
    210                     215                     220
Cys Ala Ala Glu Thr Lys Met Ser Ala Asp Asp Ala Phe Met Val Ala
225                     230                     235                     240
Pro Lys Pro Gly Leu Asp Phe Ser Pro Phe Asp Phe Ala His Phe Gly
                245                     250                     255
Phe Pro Thr Asp Asn Leu Gly Lys Asp Arg Ser Phe Leu Ala Lys Pro
            260                     265                     270
Ser Pro Lys Val Gly Arg His Val Tyr Trp Arg Pro Lys Val Asp Ile
        275                     280                     285
Lys Lys Ile Cys Ile Gly Ser Lys Asn Ile Phe Thr Val Ser Asp Leu
    290                     295                     300
Lys Pro Asn Thr Gln Tyr Tyr Phe Asp Val Phe Met Val Asn Thr Asn
305                     310                     315                     320
Thr Asn Met Asn Thr Ala Phe Val Gly Ala Phe Ala Arg Thr Lys Glu
                325                     330                     335
Glu Ala Lys Gln Lys Thr Val Glu Leu Lys Asp Gly Arg Val Thr Asp
            340                     345                     350
Val Val Val Lys Arg Lys Gly Lys Lys Phe Leu Arg Phe Ala Pro Val
        355                     360                     365
Ser Ser His Gln Lys Val Thr Leu Phe Ile His Ser Cys Met Asp Thr
    370                     375                     380
Val Gln Val Gln Val Arg Arg Asp Gly Lys Leu Leu Leu Ser Gln Asn
385                     390                     395                     400
Val Glu Gly Ile Arg Gln Phe Gln Leu Arg Gly Lys Pro Lys Gly Lys
                405                     410                     415
Tyr Leu Ile Arg Leu Lys Gly Asn Lys Lys Gly Ala Ser Met Leu Lys
            420                     425                     430
Ile Leu Ala Thr Thr Arg Pro Ser Lys His Ala Phe Pro Ser Leu Pro
        435                     440                     445
Asp Asp Thr Arg Ile Lys Ala Phe Asp Lys Leu Arg Thr Cys Ser Ser
    450                     455                     460
Val Thr Val Ala Trp Leu Gly Thr Gln Glu Arg Arg Lys Phe Cys Ile

1011c2PCTSEQUENCE LISTING
```
465                        470                        475                        480
Tyr Arg Lys Glu Val Gly Gly Asn Tyr Ser Glu Glu Gln Lys Arg Arg
                485                        490                        495
Glu Arg Asn Gln Cys Leu Gly Pro Asp Thr Arg Lys Lys Ser Glu Lys
            500                        505                        510
Val Leu Cys Lys Tyr Phe His Ser Gln Asn Leu Gln Lys Ala Val Thr
            515                        520                        525
Thr Glu Thr Ile Arg Asp Leu Gln Pro Gly Lys Ser Tyr Leu Leu Asp
        530                        535                        540
Val Tyr Val Val Gly His Gly Gly His Ser Val Lys Tyr Gln Ser Lys
545                        550                        555                        560
Leu Val Lys Thr Arg Lys Val Cys
                565
```

```
        <210> 292
        <211> 123
        <212> PRT
        <213> Mouse


        <400> 292
Met Leu Thr Glu Pro Ala Gln Leu Phe Val His Lys Lys Asn Gln Pro
    1               5                   10                  15
Pro Ser His Ser Ser Leu Arg Leu His Phe Arg Thr Leu Ala Gly Ala
                20                  25                  30
Leu Ala Leu Ser Ser Thr Gln Met Ser Trp Gly Leu Gln Ile Leu Pro
            35                  40                  45
Cys Leu Ser Leu Ile Leu Leu Leu Trp Asn Gln Val Pro Gly Leu Glu
        50                  55                  60
Gly Gln Glu Phe Arg Phe Gly Ser Cys Gln Val Thr Gly Val Val Leu
65                  70                  75                  80
Pro Glu Leu Trp Glu Ala Phe Trp Thr Val Lys Asn Thr Val Gln Thr
                85                  90                  95
Gln Asp Asp Ile Thr Ser Ile Arg Leu Leu Lys Pro Gln Val Leu Arg
                100                 105                 110
Asn Val Ser Val Ile Arg Trp Glu Gly Asp Ser
            115                 120
```

```
        <210> 293
        <211> 66
        <212> PRT
        <213> Mouse


        <400> 293
Met Asp Val Trp Ser Gly Leu Pro Leu Glu Thr Leu Trp Ile Tyr Glu
    1               5                   10                  15
Ala Val Leu Pro Trp Leu Leu Met Gly Gln Gly His Ala Trp Val Cys
                20                  25                  30
Gly Pro Ile Ala Leu Trp Val Phe Val Asn Val Pro Gly Leu Cys Tyr
            35                  40                  45
His Gln Lys Pro Phe Arg Cys Pro Trp Ser Gly Leu Leu Pro Glu Ala
        50                  55                  60
Leu Cys
65
```

```
        <210> 294
```

1011c2PCTSEQUENCE LISTING

```
<211> 294
<212> PRT
<213> Rat

<400> 294
Met Thr Val Phe Arg Lys Val Thr Thr Met Ile Ser Trp Met Leu Leu
1               5                   10                  15
Ala Cys Ala Leu Pro Cys Ala Ala Asp Pro Met Leu Gly Ala Phe Ala
            20                  25                  30
Arg Arg Asp Phe Gln Lys Gly Gly Pro Gln Leu Val Cys Ser Leu Pro
        35                  40                  45
Gly Pro Gln Gly Pro Pro Gly Pro Gly Ala Pro Gly Ser Ser Gly
    50                  55                  60
Met Val Gly Arg Met Gly Phe Pro Gly Lys Asp Gly Gln Asp Gly Gln
65                  70                  75                  80
Asp Gly Asp Arg Gly Asp Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr
                85                  90                  95
Gly Asn Arg Gly Lys Gln Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly
            100                 105                 110
Arg Ala Gly Pro Arg Gly Pro Lys Gly Val Ser Gly Thr Pro Gly Lys
        115                 120                 125
His Gly Ile Pro Gly Lys Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro
    130                 135                 140
Gly Leu Pro Gly Pro Cys Ser Cys Gly Ser Ser Arg Ala Lys Ser Ala
145                 150                 155                 160
Phe Ser Val Ala Val Thr Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile
                165                 170                 175
Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala Ser
            180                 185                 190
Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Tyr Tyr Phe Thr Tyr
        195                 200                 205
Asp Ile Thr Leu Ala Asn Lys His Leu Ala Ile Gly Leu Val His Asn
    210                 215                 220
Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn His Asp
225                 230                 235                 240
Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp Glu Val
                245                 250                 255
Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro
            260                 265                 270
Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln
        275                 280                 285
Gly Asp Pro Asn Glu Val
    290


<210> 295
<211> 243
<212> PRT
<213> Rat

<400> 295
Met Arg Pro Leu Leu Ala Leu Leu Leu Gly Leu Ala Ser Gly Ser
1               5                   10                  15
Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly Gln Pro
            20                  25                  30
Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Gln Gly Leu Pro Gly
```

1011c2PCTSEQUENCE LISTING

```
                35                        40                        45
Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu
          50                        55                        60
Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Glu Pro
 65                        70                        75                        80
Gly Pro Arg Gly Glu Ala Gly Pro Val Gly Ala Ile Gly Pro Ala Gly
                85                        90                        95
Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu
                100                       105                       110
Ser Arg Val Pro Pro Pro Ala Asp Thr Pro Leu Pro Phe Asp Arg Val
                115                       120                       125
Leu Leu Asn Glu Gln Gly His Tyr Asp Ala Thr Thr Gly Lys Phe Thr
     130                       135                       140
Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr
145                       150                       155                       160
Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Gln Ser Ile Ala
                165                       170                       175
Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser
                180                       185                       190
Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln
     195                       200                       205
Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp
     210                       215                       220
Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro
225                       230                       235                       240
Val Phe Ala
```

```
          <210> 296
          <211> 444
          <212> PRT
          <213> Rat

          <400> 296
Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
 1               5                        10                        15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
                20                        25                        30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
          35                        40                        45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
     50                        55                        60
Pro Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
 65                        70                        75                        80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
                85                        90                        95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
                100                       105                       110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
     115                       120                       125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
     130                       135                       140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
145                       150                       155                       160
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
```

1011c2PCTSEQUENCE LISTING

```
                165                        170                        175
Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
            180                   185                   190
Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
            195                   200                   205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
            210                   215                   220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys
225                   230                   235                   240
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
                245                   250                   255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
            260                   265                   270
Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp
            275                   280                   285
Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser
            290                   295                   300
Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys
305                   310                   315                   320
His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe
                325                   330                   335
Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe
                340                   345                   350
Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val
            355                   360                   365
Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val
            370                   375                   380
Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys
385                   390                   395                   400
Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys
                405                   410                   415
Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys
                420                   425                   430
Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys
            435                   440
```

```
        <210> 297
        <211> 65
        <212> PRT
        <213> Human


        <400> 297
Met Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser
1               5                   10                  15
Arg Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser
            20                  25                  30
Trp Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala
            35                  40                  45
Leu Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser
            50                  55                  60
Leu
65


        <210> 298
        <211> 52
```

1011c2PCTSEQUENCE LISTING

```
        <212> PRT
        <213> Human

        <400> 298
Met Lys Ile Asn Ile Ile Gln Gly Ser Ile Met Ile Leu Leu Ile Cys
1               5                   10                  15
Leu Ser Gln Thr Cys Thr Ser Leu Pro Val Gln Glu Ala Leu Ile Thr
            20                  25                  30
Phe Cys His Leu Tyr Phe Thr Tyr Cys Tyr Ser Gly Asn Ser Asn Lys
        35                  40                  45
Met Gln Val Leu
    50


        <210> 299
        <211> 41
        <212> PRT
        <213> Human


        <400> 299
Met Pro Cys Val Leu Phe Phe Phe Phe Phe Leu Ser Thr Ser Lys Ser
1               5                   10                  15
Met Ile Tyr Ser Ser Leu Met Leu Gly Leu Tyr Ile Pro Ser Glu Ala
            20                  25                  30
Cys Val Leu Gly Leu Lys Phe Lys Phe
        35                  40


        <210> 300
        <211> 80
        <212> PRT
        <213> Mouse


        <400> 300
Met Val Trp Gly Thr Leu Leu Gly Arg Val Leu Ala Ala Leu Leu Asn
1               5                   10                  15
Ile Val Pro Thr Glu Ser Ser Tyr Arg Ser Pro Ser Phe Leu Ala Gly
            20                  25                  30
Phe Arg Phe Cys Cys Ser Pro Trp Ser Gln His Phe Gly Cys Gly Arg
        35                  40                  45
Leu Thr Ser Cys Leu Pro Pro Cys Val Asp Arg Val Val Lys Thr Tyr
    50                  55                  60
Ser Ser Pro Pro Cys Leu Ser Val Asn Gly His Asp Val Thr Ile Cys
65                  70                  75                  80


        <210> 301
        <211> 82
        <212> PRT
        <213> Mouse


        <400> 301
Met Gly Ser Val Leu Thr Ser Cys Phe Cys Val Gly Gly Ser Ala Glu
1               5                   10                  15
Ala Trp Asn Trp Leu Pro Ser Ala Ser Ser Leu Phe Pro Cys Cys Ile
            20                  25                  30
Ala Thr Leu Leu Pro Leu Leu Phe Leu Leu Pro His Leu His Ser Thr
        35                  40                  45
```

1011c2PCTSEQUENCE LISTING
```
Leu Ser Arg Val Gln Arg Leu Asn Phe Asn Ile Gly His Leu Gly Val
    50              55              60
Tyr Leu Tyr Val Asn Asn Asp Ile Arg Ser Arg Val Thr Pro Leu Leu
65              70              75              80
Ser Ser


        <210> 302
        <211> 411
        <212> PRT
        <213> Rat


        <400> 302
Met Pro Thr Met Trp Pro Leu Leu His Val Leu Trp Leu Ala Leu Val
1               5               10              15
Cys Gly Ser Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
            20              25              30
Ala Ser Lys Thr Leu Leu Glu Lys Thr Gln Phe Ser Asp Lys Pro Val
        35              40              45
Gln Asp Arg Gly Leu Val Val Thr Asp Ile Lys Ala Glu Asp Val Val
    50              55              60
Leu Glu His Arg Ser Tyr Cys Ser Ala Arg Ala Arg Glu Arg Asn Phe
65              70              75              80
Ala Gly Glu Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr
                85              90              95
Asp Val Ala Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val
            100             105             110
Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Ile Thr Gly
    115             120             125
Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Lys Lys His Ala
    130             135             140
Lys Gly Val Arg Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr
145             150             155             160
Asp Asp Phe Arg Ser Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu
            165             170             175
Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe
            180             185             190
Val Val Glu Val Trp Ser Gln Leu Leu Ser Gln Lys His Val Gly Leu
    195             200             205
Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu
    210             215             220
Leu Val Ile Leu Val Ile Pro Pro Ala Val Thr Pro Gly Thr Asp Gln
225             230             235             240
Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Ile Leu
            245             250             255
Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ser Gln Gln Pro
            260             265             270
Gly Pro Asn Ala Pro Leu Ser Trp Ile Arg Ala Cys Val Gln Val Leu
    275             280             285
Asp Pro Lys Ser Gln Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe
    290             295             300
Tyr Gly Met Asp Tyr Ala Ala Ser Lys Asp Ala Arg Glu Pro Val Ile
305             310             315             320
Gly Ala Arg Ala Val Leu Lys Val Ala Leu Pro Leu Ala Val Ser Ser
            325             330             335
```

1011c2PCTSEQUENCE LISTING

```
Gln Gln Ile Trp Thr Leu Gly Arg Gly Gly Ser Thr Ser Ala Leu Leu
            340                     345                 350
Leu Ala Gly Leu Gly Leu Ala Ser Glu Pro Cys Thr Lys Ser Glu Glu
            355                     360                 365
Val Pro Lys Lys Ser Leu Leu Asp Thr Val Trp His Trp Gln Gly Glu
            370                     375                 380
Pro Gly Ala Leu Cys Arg Gly Arg Leu His Thr Trp Ile Leu Val Ser
385                     390                     395                 400
Ala Val Pro Gln Ala Cys Thr Cys Leu Phe Gln
                405                     410


        <210> 303
        <211> 617
        <212> PRT
        <213> Mouse


        <400> 303
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
 1               5                   10                  15
Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
            20                      25                  30
Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
            35                      40                  45
Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
            50                      55                  60
Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
65                      70                      75                  80
Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
                85                      90                  95
Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
                100                     105                 110
Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
            115                     120                 125
Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
            130                     135                 140
Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
145                     150                     155                 160
Ser Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
                165                     170                 175
Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
                180                     185                 190
Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
            195                     200                 205
Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser Trp
            210                     215                 220
Pro Glu Ala Tyr Gly Ser Asp Phe Trp Gln Ser Ile Arg Phe Thr Asp
225                     230                     235                 240
Tyr Ser Gln His Asn Gln Met Val Met Ala Leu Thr Leu Arg Cys Pro
                245                     250                 255
Leu Lys Leu Glu Ala Ser Leu Cys Trp Arg Gln Asp Pro Leu Thr Pro
                260                     265                 270
Cys Glu Thr Leu Pro Asn Ala Thr Ala Gln Glu Ser Glu Gly Trp Tyr
            275                     280                 285
Ile Leu Glu Asn Val Asp Leu His Pro Gln Leu Cys Phe Lys Phe Ser
            290                     295                 300
```

1011c2PCTSEQUENCE LISTING

```
Phe Glu Asn Ser Ser His Val Glu Cys Pro His Gln Ser Gly Ser Leu
305             310             315                 320
Pro Ser Trp Thr Val Ser Met Asp Thr Gln Ala Gln Gln Leu Thr Leu
            325             330                 335
His Phe Ser Ser Arg Thr Tyr Ala Thr Phe Ser Ala Ala Trp Ser Asp
            340             345                 350
Pro Gly Leu Gly Pro Asp Thr Pro Met Pro Pro Val Tyr Ser Ile Ser
            355             360                 365
Gln Thr Gln Gly Ser Val Pro Val Thr Leu Asp Leu Ile Ile Pro Phe
    370             375             380
Leu Arg Gln Glu Asn Cys Ile Leu Val Trp Arg Ser Asp Val His Phe
385             390             395                 400
Ala Trp Lys His Val Leu Cys Pro Asp Asp Ala Pro Tyr Pro Thr Gln
            405             410                 415
Leu Leu Leu Arg Ser Leu Gly Ser Gly Arg Thr Arg Pro Val Leu Leu
            420             425                 430
Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly Ala Leu
    435             440                 445
Ala Glu Leu Leu Arg Thr Ala Leu Gly Gly Gly Arg Asp Val Ile Val
    450             455                 460
Asp Leu Trp Glu Gly Thr His Val Ala Arg Ile Gly Pro Leu Pro Trp
465             470             475                 480
Leu Trp Ala Ala Arg Glu Arg Val Ala Arg Glu Gln Gly Thr Val Leu
            485             490                 495
Leu Leu Trp Asn Cys Ala Gly Pro Ser Thr Ala Cys Ser Gly Asp Pro
            500             505                 510
Gln Ala Ala Ser Leu Arg Thr Leu Leu Cys Ala Ala Pro Arg Pro Leu
    515             520                 525
Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp Ile Pro Arg
    530             535                 540
Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp Leu Pro Arg
545                 550             555                 560
Leu Leu Arg Ala Leu Asp Ala Gln Pro Ala Thr Leu Ala Ser Ser Trp
            565             570                 575
Ser His Leu Gly Ala Lys Arg Cys Leu Lys Asn Arg Leu Glu Gln Cys
            580             585                 590
His Leu Leu Glu Leu Glu Ala Ala Lys Asp Asp Tyr Gln Gly Ser Thr
            595             600                 605
Asn Ser Pro Cys Gly Phe Ser Cys Leu
    610             615
```

```
        <210> 304
        <211> 72
        <212> PRT
        <213> Mouse


        <400> 304
Met Ser Ala Ile Phe Asn Phe Gln Ser Leu Leu Thr Val Ile Leu Leu
1               5               10                  15
Leu Ile Cys Thr Cys Ala Tyr Ile Arg Ser Leu Ala Pro Ser Ile Leu
            20              25                  30
Asp Arg Asn Lys Thr Gly Leu Leu Gly Ile Phe Trp Lys Cys Ala Arg
            35              40                  45
Ile Gly Glu Arg Lys Ser Pro Tyr Val Ala Ile Cys Cys Ile Val Met
    50              55                  60
```

1011c2PCTSEQUENCE LISTING

Ala Phe Ser Ile Leu Phe Ile Gln
65                70

```
        <210> 305
        <211> 649
        <212> PRT
        <213> Mouse


        <400> 305
```

Met Ile Ser Pro Ala Trp Ser Leu Phe Leu Ile Gly Thr Lys Ile Gly
1             5             10            15
Leu Phe Phe Gln Val Ala Pro Leu Ser Val Val Ala Lys Ser Cys Pro
            20            25            30
Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Ser
            35            40            45
Leu Thr Ser Ile Pro Val Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr
            50            55            60
Leu Gln Asn Asn Gln Ile Asn Asn Val Gly Ile Pro Ser Asp Leu Lys
65                70            75                80
Asn Leu Leu Lys Val Gln Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp
            85            90            95
Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln
            100           105           110
Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro
            115           120           125
Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser
            130           135           140
Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe
145           150           155           160
Leu Ser Arg Asn His Leu Ser Thr Ile Pro Gly Gly Leu Pro Arg Thr
            165           170           175
Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser
            180           185           190
Pro Ser Leu His Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly
            195           200           205
Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu
            210           215           220
Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala
225           230           235           240
Pro Val Asn Leu Pro Gly Thr Ser Leu Arg Lys Leu Tyr Leu Gln Asp
            245           250           255
Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln
            260           265           270
Leu Tyr Arg Leu Asp Met Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln
            275           280           285
Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn
            290           295           300
Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu
305           310           315           320
Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala
            325           330           335
Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Ser Ala Glu Leu
            340           345           350
Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr
            355           360           365

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1011c2PCTSEQUENCE LISTING

```
Ala Ile Pro Asn Thr Ala Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro
    370             375         380
Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Ile Lys Asp Gln
385             390         395                 400
Arg Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Leu Ile Thr Val Lys
            405         410                 415
Ser Val Thr Pro Asp Thr Ile His Ile Ser Trp Arg Leu Ala Leu Pro
            420         425                 430
Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala
        435             440                 445
Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr
        450             455                 460
Leu Val Thr Ala Leu Glu Pro Glu Ser Pro Tyr Arg Val Cys Met Val
465             470                 475                 480
Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys
                485             490                 495
Ile Glu Thr Gln Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr
            500             505                 510
Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro
        515             520                 525
Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Ser Ile Ala Leu
        530             535                 540
Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser
545             550             555                 560
Arg Asn Cys Ala Tyr Ser Lys Gly Arg Arg Arg Lys Asp Asp Tyr Ala
            565             570                 575
Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr
            580             585                 590
Ser Phe Gln Met Leu Pro Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu
        595             600                 605
Phe Val Ile His Thr Ile Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys
610                 615                 620
Asn Asn Leu Ser Glu Ser Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly
625             630             635                 640
Ile Pro Asp Ser Asp His Ser His Ser
            645
```

        <210> 306
        <211> 150
        <212> PRT
        <213> Rat


        <400> 306

```
Met Ala Ala Pro Met Asp Arg Thr His Gly Gly Arg Ala Ala Arg Ala
 1             5             10                 15
Leu Arg Arg Ala Leu Ala Leu Ala Ser Leu Ala Gly Leu Leu Leu Ser
            20             25                 30
Gly Leu Ala Gly Ala Leu Pro Thr Leu Gly Pro Gly Trp Arg Arg Gln
        35             40                 45
Asn Pro Glu Pro Pro Ala Ser Arg Thr Arg Ser Leu Leu Leu Asp Ala
    50             55                 60
Ala Ser Gly Gln Leu Arg Leu Glu Tyr Gly Phe His Pro Asp Ala Val
65             70             75                 80
Ala Trp Ala Asn Leu Thr Asn Ala Ile Arg Glu Thr Gly Trp Ala Tyr
            85             90                 95
```

1011c2PCTSEQUENCE LISTING

```
Leu Asp Leu Gly Thr Asn Gly Ser Tyr Lys Trp Ile Pro Arg Ala Ala
             100                 105                 110
Gly Leu Cys Ser Trp Cys Gly Gly Gly Leu Cys Val Arg Gly Ala His
             115                 120                 125
Leu His Ala Leu Asp Glu His Gly Gly Gln Leu Leu Arg Pro Leu Arg
             130                 135                 140
Val Arg Ser Arg Leu Leu
145                 150


        <210> 307
        <211> 580
        <212> PRT
        <213> Rat


        <400> 307
Met Ala Ala Ala Met Pro Leu Gly Leu Ser Leu Leu Leu Leu Val Leu
  1               5              10                  15
Val Gly Gln Gly Cys Cys Gly Arg Val Glu Gly Pro Arg Asp Ser Leu
             20                  25                  30
Arg Glu Glu Leu Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala
             35                  40                  45
Thr Phe Gln Phe Arg Thr Arg Trp Asp Ser Asp Leu Gln Arg Glu Gly
   50                  55                  60
Val Ser His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser
65                  70                  75                  80
Lys Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
                85                  90                  95
Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly Ala
             100                 105                 110
Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp Lys Ser
             115                 120                 125
Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys Ala Ser Leu
             130                 135                 140
Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr Ala Ser Phe Lys
145                 150                 155                 160
Pro Leu Gly Leu Ala Asn Asp Thr Asp His Tyr Phe Leu Arg Tyr Ala
                   165                 170                 175
Val Leu Pro Arg Glu Val Val Cys Thr Glu Asn Leu Thr Pro Trp Lys
             180                 185                 190
Lys Leu Leu Pro Cys Ser Ser Lys Ala Gly Leu Ser Val Leu Leu Lys
             195                 200                 205
Ala Asp Arg Leu Phe His Thr Ser Tyr His Ser Gln Ala Val His Ile
             210                 215                 220
Arg Pro Ile Cys Arg Asn Ala His Cys Thr Ser Ile Ser Trp Glu Leu
225                 230                 235                 240
Arg Gln Thr Leu Ser Val Val Phe Asp Ala Phe Ile Thr Gly Gln Gly
                   245                 250                 255
Lys Lys Asp Trp Ser Leu Phe Arg Met Phe Ser Arg Thr Leu Thr Glu
             260                 265                 270
Ala Cys Pro Leu Ala Ser Gln Ser Leu Val Tyr Val Asp Ile Thr Gly
             275                 280                 285
Tyr Ser Gln Asp Asn Glu Thr Leu Glu Val Ser Pro Pro Pro Thr Ser
             290                 295                 300
Thr Tyr Gln Asp Val Ile Leu Gly Thr Arg Lys Thr Tyr Ala Val Tyr
305                 310                 315                 320
```

1011c2PCTSEQUENCE LISTING

```
Asp Leu Phe Asp Thr Ala Met Ile Asn Asn Ser Arg Asn Leu Asn Ile
             325                 330                 335
Gln Leu Lys Trp Lys Arg Pro Pro Asp Asn Glu Ala Leu Pro Val Pro
             340                 345                 350
Phe Leu His Ala Gln Arg Tyr Val Ser Gly Tyr Gly Leu Gln Lys Gly
             355                 360                 365
Glu Leu Ser Thr Leu Leu Tyr Asn Ser His Pro Tyr Arg Ala Phe Pro
         370                 375                 380
Val Leu Leu Leu Asp Ala Val Pro Trp Tyr Leu Arg Leu Tyr Val His
385                 390                 395                 400
Thr Leu Thr Ile Thr Ser Lys Gly Lys Asp Asn Lys Pro Ser Tyr Ile
                 405                 410                 415
His Tyr Gln Pro Ala Gln Asp Arg Gln Gln Pro His Leu Leu Glu Met
             420                 425                 430
Leu Ile Gln Leu Pro Ala Asn Ser Val Thr Lys Val Ser Ile Gln Phe
             435                 440                 445
Glu Arg Ala Leu Leu Lys Trp Thr Glu Tyr Thr Pro Asp Pro Asn His
         450                 455                 460
Gly Phe Tyr Val Ser Pro Ser Val Leu Ser Ala Leu Val Pro Ser Met
465                 470                 475                 480
Val Ala Ala Lys Pro Val Asp Trp Glu Glu Ser Pro Leu Phe Asn Thr
                 485                 490                 495
Leu Phe Pro Val Ser Asp Gly Ser Ser Tyr Phe Val Arg Leu Tyr Thr
             500                 505                 510
Glu Pro Leu Leu Val Asn Leu Pro Thr Pro Asp Phe Ser Met Pro Tyr
             515                 520                 525
Asn Val Ile Cys Leu Thr Cys Thr Val Val Ala Val Cys Tyr Gly Ser
         530                 535                 540
Phe Tyr Asn Leu Leu Thr Arg Thr Phe His Ile Glu Glu Pro Lys Ser
545                 550                 555                 560
Gly Gly Leu Ala Lys Arg Leu Ala Asn Leu Ile Arg Arg Ala Arg Gly
                 565                 570                 575
Val Pro Pro Leu
             580


            <210> 308
            <211> 283
            <212> PRT
            <213> Rat


            <400> 308
Met Thr Ser Gly Pro Gly Gly Pro Ala Ala Ala Thr Gly Gly Gly Lys
  1           5                 10                  15
Asp Thr His Gln Trp Tyr Val Cys Asn Arg Glu Lys Leu Cys Glu Ser
             20                  25                  30
Leu Gln Ser Val Phe Val Gln Ser Tyr Leu Asp Gln Gly Thr Gln Ile
             35                  40                  45
Phe Leu Asn Asn Ser Ile Glu Lys Ser Gly Trp Leu Phe Ile Gln Leu
         50                  55                  60
Tyr His Ser Phe Val Ser Ser Val Phe Ser Leu Phe Met Ser Arg Thr
65                  70                  75                  80
Ser Ile Asn Gly Leu Leu Gly Arg Gly Ser Met Phe Val Phe Ser Pro
                 85                  90                  95
Asp Gln Phe Gln Arg Leu Leu Lys Ile Asn Pro Asp Trp Lys Thr His
             100                 105                 110
```

1011c2PCTSEQUENCE LISTING

Arg Leu Leu Asp Leu Gly Ala Gly Asp Gly Glu Val Thr Lys Ile Met
        115                 120                 125
Ser Pro His Phe Glu Glu Ile Tyr Ala Thr Glu Leu Ser Glu Thr Met
        130                 135                 140
Ile Trp Gln Leu Gln Lys Lys Lys Tyr Arg Val Leu Gly Ile Asn Glu
145                 150                 155                 160
Trp Gln Asn Thr Gly Phe Gln Tyr Asp Val Ile Ser Cys Leu Asn Leu
                165                 170                 175
Leu Asp Arg Cys Asp Gln Pro Leu Thr Leu Leu Lys Asp Ile Arg Ser
            180                 185                 190
Val Leu Glu Pro Thr Gln Gly Arg Val Ile Leu Ala Leu Val Leu Pro
        195                 200                 205
Phe His Pro Tyr Val Glu Asn Val Gly Gly Lys Trp Glu Lys Pro Ser
    210                 215                 220
Glu Ile Leu Glu Ile Lys Gly Gln Asn Trp Glu Glu Gln Val Asn Ser
225                 230                 235                 240
Leu Pro Glu Val Phe Arg Lys Ala Gly Phe Val Ile Glu Ala Phe Thr
            245                 250                 255
Arg Leu Pro Tyr Leu Cys Glu Gly Asp Met Tyr Asn Asp Tyr Tyr Val
            260                 265                 270
Leu Asp Asp Ala Val Phe Val Leu Arg Pro Val
            275                 280

        <210> 309
        <211> 37
        <212> PRT
        <213> Rat

        <400> 309
Met Leu Trp Val Leu Leu Ser Leu Thr Pro Leu Leu Ser Pro Leu Ile
1               5                 10                  15
Phe Phe Pro Val Lys Thr Val Ala Leu Glu Glu Ile Ser Thr Ile Cys
            20                  25                  30
Arg Ala Asp Val Leu
        35

        <210> 310
        <211> 70
        <212> PRT
        <213> Mouse

        <400> 310
Met Ala Ala Ser Trp Gly Gln Val Leu Ala Leu Val Leu Val Ala Ala
1               5                 10                  15
Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys Arg Ala Ser Ser Gly Leu
            20                  25                  30
Glu Gln Val Arg Glu Arg Thr Trp Ala Trp Gln Leu Leu Gln Glu Ile
        35                  40                  45
Lys Ala Leu Phe Gly Asn Thr Glu Val Arg Leu Ala Leu Thr Asp Glu
    50                  55                  60
Pro Leu Lys Ile Ser Pro
65              70

        <210> 311
        <211> 58

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1011c2PCTSEQUENCE LISTING
```
        <212> PRT
        <213> Human

        <400> 311
Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu Ala
1                   5                   10                  15
Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys Ile Thr
            20                  25                  30
Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe Arg Lys Val
        35                  40                  45
Gln Glu Pro Gln Gly Lys Ala Lys Arg His
    50                  55


        <210> 312
        <211> 52
        <212> PRT
        <213> Human

        <400> 312
Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys
1                   5                   10                  15
Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser
            20                  25                  30
Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu
        35                  40                  45
Glu Lys Thr Lys
    50


        <210> 313
        <211> 70
        <212> PRT
        <213> Human

        <400> 313
Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
1                   5                   10                  15
Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
            20                  25                  30
Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
        35                  40                  45
Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
    50                  55                  60
Pro Met Thr Pro Pro Trp
65                  70


        <210> 314
        <211> 58
        <212> PRT
        <213> Mouse

        <400> 314
Met Phe Ile Thr Pro Phe Lys Ala Phe Leu Pro Leu Tyr Leu Leu Thr
1                   5                   10                  15
Glu Leu Ser Leu Ile Asp Ile Thr Ser Cys Asp Asp Leu Pro His Ser
            20                  25                  30
```

1011c2PCTSEQUENCE LISTING

```
Val Leu Pro Gln His Leu Ser Phe Glu Phe Val Leu Trp Ser Met Tyr
        35              40                  45
Leu Leu Ile Cys Cys Phe Val Ile Ile Phe
    50              55
```

```
<210> 315
<211> 229
<212> PRT
<213> Rat
```

```
<400> 315
Met Ala Ser Ala Leu Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys
1               5               10                  15
Val Leu Leu Glu Lys Ser Thr Arg Lys Arg Leu Arg Asp Thr Leu Thr
            20              25                  30
Asn Glu Lys Ser Lys Ile Glu Thr Glu Leu Arg Asn Lys Met Gln Gln
        35              40                  45
Lys Ser Gln Lys Lys Pro Glu Phe Asp Asn Glu Lys Pro Ala Ala Val
    50              55                  60
Val Ala Pro Leu Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly
65              70                  75                  80
Trp Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly
            85              90                  95
Val His Gln Val Pro Ala Glu Asn Val Gln Val His Phe Thr Glu Arg
            100             105                 110
Ser Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Asn Tyr Ser Met
            115             120                 125
Ile Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Ser Ser Ser Lys
    130             135                 140
Lys Val Lys Thr Asp Thr Val Ile Ile Leu Cys Arg Lys Lys Ala Glu
145             150                 155                 160
Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu
            165             170                 175
Lys Glu Lys Pro Ser Tyr Asp Thr Glu Ala Asp Pro Ser Glu Gly Leu
            180             185                 190
Met Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys
            195             200                 205
Arg Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Arg
210             215                 220
Glu Asp Thr Glu Phe
225
```

```
<210> 316
<211> 128
<212> PRT
<213> Rat
```

```
<400> 316
Arg Ala Glu Phe Gly Thr Ser Gly Glu Met Gly Asn Ala Ala Leu Gly
1           ·   5               10                  15
Ala Glu Leu Gly Val Arg Val Leu Leu Phe Val Ala Phe Leu Ala Thr
            20              25                  30
Glu Leu Leu Pro Pro Phe Gln Arg Arg Ile Gln Pro Glu Glu Leu Trp
        35              40                  45
Leu Tyr Arg Asn Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Gly Pro
```

P

1011c2PCTSEQUENCE LISTING

```
        50                    55                    60
Met Phe Val Ile Ala Phe Leu Thr Pro Leu Ser Leu Ile Phe Phe Ala
65                    70                    75                    80
Lys Phe Leu Arg Lys Ala Asp Ala Thr Asp Ser Lys Gln Ala Cys Leu
                85                    90                    95
Ala Ala Ser Leu Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Ile Ile
              100                   105                   110
Lys Leu Ile Val Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe
            115                   120                   125
```

```
        <210> 317
        <211> 75
        <212> PRT
        <213> Rat

        <400> 317
Ser Ala Gly Val Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile
1                   5                   10                    15
Ala Phe Gly Pro Ala Leu Ser Leu Tyr Val Phe Thr Ile Ala Thr Asp
                20                    25                    30
Pro Leu Arg Val Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val
            35                    40                    45
Ser Leu Leu Leu Ser Ser Val Phe Trp Phe Leu Val Arg Val Ile Thr
            50                    55                    60
Asp Asn Arg Asp Gly Pro Val Gln Asn Tyr Leu
65                    70                    75
```

```
        <210> 318
        <211> 43
        <212> PRT
        <213> Human

        <400> 318
Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe Cys
1                   5                   10                    15
Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys Gly Glu
                20                    25                    30
Ser Arg Thr Pro Arg Pro Thr Ala Leu Gly Asn
            35                    40
```

```
        <210> 319
        <211> 86
        <212> PRT
        <213> Mouse

        <400> 319
Met Leu Gln Gly Pro Ala Pro Ser Cys Phe Trp Val Phe Ser Gly Ile
1                   5                   10                    15
Cys Val Phe Trp Asp Phe Ile Phe Ile Ile Phe Phe Asn Val Leu Ser
                20                    25                    30
Leu Gly Asn Arg Glu Ile Ser Ala Lys Asp Phe Ala Asp Gln Pro Ala
            35                    40                    45
Gly Ala Gln Gly Met Trp Gly Ile Trp Gly His Thr Ile Thr Cys Gly
            50                    55                    60
Leu Ala Pro Gly Ala Lys Pro Cys Ser Leu Lys Arg Glu Gly Pro Asp
```

1011c2PCTSEQUENCE LISTING
65                          70                          75                          80
Leu Leu Ser Phe Pro Pro
                    85


    <210> 320
    <211> 60
    <212> PRT
    <213> Mouse


    <400> 320
Lys Gly Pro Glu Val Ser Cys Cys Ile Lys Tyr Phe Ile Phe Gly Phe
1                   5                   10                  15
Asn Val Ile Phe Trp Phe Leu Gly Ile Thr Phe Leu Gly Ile Gly Leu
            20                  25                  30
Trp Ala Trp Asn Glu Lys Gly Val Leu Ser Asn Ile Ser Ser Ile Thr
            35                  40                  45
Asp Leu Gly Gly Phe Asp Pro Val Trp Leu Phe Leu
    50                  55                  60


    <210> 321
    <211> 160
    <212> PRT
    <213> Mouse


    <400> 321
Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala
1                   5                   10                  15
Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu
            20                  25                  30
Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro
    35                  40                  45
Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu
    50                  55                  60
Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu
65                  70                  75                  80
Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly
                85                  90                  95
Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe
            100                 105                 110
Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val
    115                 120                 125
Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr
    130                 135                 140
Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Ser Ser
145                 150                 155                 160


    <210> 322
    <211> 54
    <212> PRT
    <213> Mouse


    <400> 322
Arg Leu Gln Val Asp Thr Ser Gly Ser Lys Val Leu Phe Leu Phe Phe
1                   5                   10                  15
Phe Phe Phe Leu Cys Val Cys Val Leu Val Cys Cys Cys Phe Gly Phe

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10.11c2PCTSEQUENCE LISTING

```
                20                    25                    30
Pro Gly Thr His Ser Val Asp Gln Ala Ser Pro Lys Leu Arg Asn Leu
        35                    40                    45
Pro Pro Glu Cys Trp Asp
    50
```

<210> 323
<211> 280
<212> PRT
<213> Mouse

<400> 323

```
Leu Asp Ser Arg Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser
1               5               10                    15
Ala Arg Glu Asn Ile Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile
            20                    25                    30
Val Phe Ala Ile Phe Met Ala Ala Glu Thr Phe Thr Asp Ile Phe Ile
            35                    40                    45
Ser Trp Ser Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro
    50                    55                    60
His His His His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu
65                    70                    75                    80
Leu Thr His Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val
            85                    90                    95
Leu Trp Leu Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg
            100                   105                   110
Lys Phe Val His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala
            115                   120                   125
Cys Ile Val Gln Ala Lys Glu Arg Ser Tyr Glu Thr Met Leu Ser Phe
    130                   135                   140
Gly Lys Arg Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala
145                   150                   155                   160
Thr Lys Ser Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met
            165                   170                   175
Gln Asp Leu Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp
            180                   185                   190
Pro Leu Tyr Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly
            195                   200                   205
Tyr Arg Pro Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp
    210                   215                   220
Ser Asp Asn Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys
225                   230                   235                   240
Pro Leu Gly Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu
            245                   250                   255
Thr Arg Glu Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys
            260                   265                   270
Ala Met Pro Ser Asp Met Asp Ser
            275                   280
```

<210> 324
<211> 166
<212> PRT
<213> Rat

<400> 324

1011c2PCTSEQUENCE LISTING

```
Ala Leu Arg Arg Val Gly Met Glu Leu Pro Ala Val Asn Leu Lys Val
1               5               10                  15
Ile Leu Leu Val His Trp Leu Leu Thr Thr Trp Gly Cys Leu Ala Phe
            20              25                  30
Ser Gly Ser Tyr Ala Trp Gly Asn Phe Thr Ile Leu Ala Leu Gly Val
        35              40                  45
Trp Ala Val Ala Gln Arg Asp Ser Val Asp Ala Ile Gly Met Phe Leu
    50              55                  60
Gly Gly Leu Val Ala Thr Ile Phe Leu Asp Ile Ile Tyr Ile Ser Ile
65              70                  75                  80
Phe Tyr Ser Ser Val Ala Val Gly Asp Thr Gly Arg Phe Ser Ala Gly
                85              90                  95
Met Ala Ile Phe Ser Leu Leu Leu Lys Pro Phe Ser Cys Cys Leu Val
            100             105                 110
Tyr His Met His Arg Glu Arg Gly Gly Glu Leu Pro Leu Arg Ser Asp
    115             120                 125
Phe Phe Gly Pro Ser Gln Glu His Ser Ala Tyr Gln Thr Ile Asp Ser
    130             135                 140
Ser Asp Ser Pro Ala Asp Pro Leu Ala Ser Leu Glu Asn Lys Gly Gln
145             150                 155                 160
Ala Ala Pro Arg Gly Tyr
                165
```

```
        <210> 325
        <211> 338
        <212> PRT
        <213> Rat

        <400> 325
Ile Arg His Glu Ala Glu Ala Gly Arg His Gln Pro Glu Gln Leu Ala
1               5               10                  15
Ala Asp Ser Arg Thr Glu Thr Val Gly Pro Arg Gln Ser Asn Gly Leu
            20              25                  30
Thr Gly Pro Gly Leu Pro Thr Trp Gln Leu His Pro Val Leu Phe Pro
        35              40                  45
Glu Leu Val Leu Trp Val Asn Met Val Pro Cys Phe Leu Leu Ser Leu
    50              55                  60
Leu Leu Leu Val Arg Pro Ala Pro Val Val Ala Tyr Ser Val Ser Leu
65              70                  75                  80
Pro Ala Ser Phe Leu Glu Glu Val Ala Gly Ser Gly Glu Ala Glu Gly
                85              90                  95
Ser Ser Ala Ser Ser Pro Ser Leu Leu Pro Pro Arg Thr Pro Ala Phe
            100             105                 110
Ser Pro Thr Pro Gly Arg Thr Gln Pro Thr Ala Pro Val Gly Pro Val
    115             120                 125
Pro Pro Thr Asn Leu Leu Asp Gly Ile Val Asp Phe Phe Arg Gln Tyr
    130             135                 140
Val Met Leu Ile Ala Val Val Gly Ser Leu Thr Phe Leu Ile Met Phe
145             150                 155                 160
Ile Val Cys Ala Ala Leu Ile Thr Arg Gln Lys His Lys Ala Thr Ala
            165             170                 175
Tyr Tyr Pro Ser Ser Phe Pro Glu Lys Lys Tyr Val Asp Gln Arg Asp
            180             185                 190
Arg Ala Gly Gly Pro His Ala Phe Ser Glu Val Pro Asp Arg Ala Pro
        195             200                 205
```

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1011c2PCTSEQUENCE LISTING

```
Asp Ser Arg Gln Glu Glu Gly Leu Asp Ser Ser Gln Gln Leu Gln Ala
210               215               220
Asp Ile Leu Ala Ala Thr Gln Asn Leu Arg Ser Pro Ala Arg Ala Leu
225               230               235               240
Pro Gly Ser Gly Glu Gly Thr Lys Gln Val Lys Gly Gly Ser Glu Glu
            245               250               255
Glu Glu Glu Lys Glu Glu Glu Val Phe Ser Gly Gln Glu Glu Pro Arg
            260               265               270
Glu Ala Pro Val Cys Gly Val Thr Glu Glu Lys Pro Glu Val Pro Asp
            275               280               285
Glu Thr Ala Ser Ala Glu Ala Glu Gly Val Pro Ala Ala Ser Glu Gly
            290               295               300
Gln Gly Glu Pro Glu Gly Ser Phe Ser Leu Ala Gln Glu Pro Gln Gly
305               310               315               320
Ala Ala Gly Pro Ser Glu Arg Ser Cys Ala Cys Asn Arg Ile Ser Pro
            325               330               335
Asn Val
```

```
<210> 326
<211> 347
<212> PRT
<213> Human

<400> 326
Ala Trp Ser Arg Pro Arg Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala
1                5                10               15
Trp Gly Ile Val Leu Glu Thr Val Ala Thr Ala Gly Val Val Thr Ser
            20               25               30
Val Ala Phe Met Leu Thr Leu Pro Ile Leu Val Cys Lys Val Gln Asp
            35               40               45
Ser Asn Arg Arg Lys Met Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly
            50               55               60
Val Leu Gly Ile Phe Gly Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp
65               70               75               80
Gly Ser Thr Gly Pro Thr Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser
                85               90               95
Ile Cys Phe Ser Cys Leu Leu Ala His Ala Val Ser Leu Thr Lys Leu
            100              105              110
Val Arg Gly Arg Lys Pro Leu Ser Leu Leu Val Ile Leu Gly Leu Ala
            115              120              125
Val Gly Phe Ser Leu Val Gln Asp Val Ile Ala Ile Glu Tyr Ile Val
            130              135              140
Leu Thr Met Asn Arg Thr Asn Val Asn Val Phe Ser Glu Leu Ser Ala
145              150              155              160
Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Leu Thr Tyr Val Leu Phe
            165              170              175
Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser
            180              185              190
Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu
            195              200              205
Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro
210              215              220
Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala
225              230              235              240
```

1011c2PCTSEQUENCE LISTING

```
Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp
            245             250             255
Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala
            260             265             270
Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg
            275             280             285
Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp
    290             295             300
Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro
305             310             315             320
Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser Pro
            325             330             335
Tyr Lys Asp Tyr Glu Val Lys Lys Glu Gly Ser
            340             345
```

        <210> 327
        <211> 141
        <212> PRT
        <213> Human


        <400> 327

```
Lys Asn Ser Lys Cys Leu Leu Phe Trp Cys Arg Lys Ile Val Gly Asn
1               5               10              15
Arg Gln Glu Pro Met Trp Glu Phe Asn Phe Lys Phe Lys Lys Gln Ser
            20              25              30
Pro Arg Leu Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln
        35              40              45
Tyr Glu Asp Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln
    50              55              60
Val Thr Thr Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile
65              70              75              80
Phe Thr Leu Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg
            85              90              95
Val Arg Leu Val Phe Gln Asp Ser Pro Val His Gly Gly Arg Lys Leu
            100             105             110
Arg Ser Glu Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe
            115             120             125
Gly Ser Leu Thr Gly Gly Ile Leu Ser Thr His Ser Pro
    130             135             140
```

        <210> 328
        <211> 71
        <212> PRT
        <213> Human


        <400> 328

```
Arg Glu Arg Thr Ser Leu Glu Phe Phe Val Phe Leu Phe Leu Phe Ile
1               5               10              15
Cys Cys Cys Leu His Ser Gly Gly Leu Gly Gly Val Pro Leu Pro Pro
            20              25              30
Phe Pro Pro Gln Ala Gln Arg Gly Glu Gly Pro Gly Lys Trp Met Ser
        35              40              45
Pro Pro Leu Pro Pro His Pro Val Val Ala Pro Pro Thr Pro Ser Pro
    50              55              60
Ser Arg Gly Cys Val Leu Leu
```

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1011c2PCTSEQUENCE LISTING
65                        70

```
            <210> 329
            <211> 109
            <212> PRT
            <213> Human


            <400> 329
Asp Gly Pro Ser Pro Lys Leu Ala Leu Trp Leu Pro Ser Pro Ala Pro
1               5                   10                  15
Thr Ala Ala Pro Thr Ala Leu Gly Glu Ala Gly Leu Ala Glu His Ser
                20                  25                  30
Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
        35                  40                  45
Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
        50                  55                  60
Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
65                  70                  75                  80
Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu Pro Met Pro Pro Arg
                85                  90                  95
Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
                100                 105
```

```
            <210> 330
            <211> 155
            <212> PRT
            <213> Human


            <400> 330
Ser Val Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu
1               5                   10                  15
Ala Ala Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu
                20                  25                  30
Ser Ser Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys
        35                  40                  45
Arg Pro Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu
        50                  55                  60
Asp Glu Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys
65                  70                  75                  80
Asp Pro Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly
                85                  90                  95
Val Ser Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro
                100                 105                 110
Asp Tyr Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val
        115                 120                 125
Lys Tyr Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe
        130                 135                 140
Asp Pro Ser Lys Ile Gln Leu Pro Glu Asp Glu
145                 150                 155
```

```
            <210> 331
            <211> 299
            <212> PRT
            <213> Human
```

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1011c2PCTSEQUENCE LISTING

&lt;400&gt; 331

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Gly | Thr | Lys | Ala | Gln | Val | Glu | Arg | Lys | Leu | Leu | Cys | Leu | Phe | Ile |

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
1               5                   10                  15
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
            20              25                  30
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
        35                  40                  45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
    50                  55                  60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65              70                  75                      80
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
            85                  90                  95
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
            100                 105                 110
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
            115                 120                 125
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
    130                 135                 140
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
145                 150                 155                 160
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
            165                 170                 175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
            180                 185                 190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
            195                 200                 205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
    210                 215                 220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225                 230                 235                 240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
            245                 250                 255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
            260                 265                 270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
            275                 280                 285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290                 295

&lt;210&gt; 332
&lt;211&gt; 299
&lt;212&gt; PRT
&lt;213&gt; Mouse

&lt;400&gt; 332

Ala Arg Ala Gly Ala Cys Tyr Cys Pro Ala Gly Phe Leu Gly Ala Asp
1               5                   10                  15
Cys Ser Leu Ala Cys Pro Gln Gly Arg Phe Gly Pro Ser Cys Ala His
            20                  25                  30
Val Cys Thr Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr
            35                  40                  45
Cys Ile Cys Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys
    50                  55                  60
Pro Gln Asp Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg

1011c2PCTSEQUENCE LISTING

```
65                          70                      75                      80
Asn Gly Gly Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu
                85                      90                      95
Gly Trp Met Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr
                100                     105                     110
Gly Ala Ala Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys
        115                     120                     125
Glu Pro Thr Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln
    130                     135                     140
Ala Cys Glu Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln
145                     150                     155                     160
Arg Val Cys Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly
                165                     170                     175
Arg Cys Leu Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly
            180                     185                     190
Cys Lys Pro Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys
            195                     200                     205
Pro Thr Gly Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro
    210                     215                     220
Pro Gly Arg Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg
225                     230                     235                     240
Phe Gly Pro Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp
                245                     250                     255
Cys Asp Pro Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly
            260                     265                     270
Pro Thr Cys Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala
            275                     280                     285
Pro Gln His Ser Ser Ser Lys Ala Met Lys His
    290                     295
```

```
            <210> 333
            <211> 109
            <212> PRT
            <213> Mouse


            <400> 333
Gly Thr Arg Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
1                   5                   10                      15
Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
                20                      25                      30
Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
        35                      40                      45
Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
    50                      55                      60
Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile
65                      70                      75                      80
Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr
                85                      90                      95
Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Thr
            100                     105
```

```
            <210> 334
            <211> 787
            <212> PRT
            <213> Mouse
```

1011c2PCTSEQUENCE LISTING

<400> 334

| Lys 1 | Val | Glu | Gly | Glu 5 | Gly | Arg | Gly | Arg | Trp 10 | Ala | Leu | Gly | Leu | Leu 15 | Arg |

Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
1              5                    10                      15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
         20              25                    30
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
         35              40                    45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
    50              55                    60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
65              70                    75                      80
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
             85                    90                      95
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
         100                   105                   110
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
         115                   120                   125
Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp
    130                   135                   140
Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile
145                   150                   155                   160
Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp
             165                   170                   175
Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu
         180                   185                   190
Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr
         195                   200                   205
Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe
    210                   215                   220
Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly
225                   230                   235                   240
His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys
             245                   250                   255
Ala Ser Leu Ile Gly Leu Met Gln Arg Cys Trp His Ala Asp Pro Gln
         260                   265                   270
Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys
         275                   280                   285
Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu
    290                   295                   300
Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser Arg
305                   310                   315                   320
Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu Ser
             325                   330                   335
Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Ser Gln Thr Leu Glu Gly
         340                   345                   350
Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Cys Lys Leu Pro Ser Ser
         355                   360                   365
Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala Phe
    370                   375                   380
Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala Ser Thr
385                   390                   395                   400
Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala
             405                   410                   415
Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln

1011c2PCTSEQUENCE LISTING

```
                420                      425                       430
Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala
            435                      440                      445
Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn
            450                      455                      460
Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met
465                      470                      475                      480
Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg
                485                      490                      495
Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His
                500                      505                      510
Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Leu Glu
            515                      520                      525
Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met
            530                      535                      540
His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu
545                      550                      555                      560
Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro
                565                      570                      575
Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu Leu
            580                      585                      590
Ala Lys Gln Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly Arg
            595                      600                      605
Thr Pro Leu His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala Arg
            610                      615                      620
Ile Leu Ile Asp Leu Cys Ser Asp Val Asn Ile Cys Ser Leu Gln Ala
625                      630                      635                      640
Gln Thr Pro Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr Ala
                645                      650                      655
Arg Leu Leu Leu His Arg Gly Ala Gly Lys Glu Ala Leu Thr Ser Glu
            660                      665                      670
Gly Tyr Thr Ala Leu His Leu Ala Ala Gln Asn Gly His Leu Ala Thr
            675                      680                      685
Val Lys Leu Leu Ile Glu Glu Lys Ala Asp Val Met Ala Arg Gly Pro
            690                      695                      700
Leu Asn Gln Thr Ala Leu His Leu Ala Ala Ala Arg Gly His Ser Glu
705                      710                      715                      720
Val Val Glu Glu Leu Val Ser Ala Asp Leu Ile Asp Leu Ser Asp Glu
                725                      730                      735
Gln Gly Leu Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ser Gln
            740                      745                      750
Thr Val Glu Thr Leu Leu Lys His Gly Ala His Ile Asn Leu Gln Ser
            755                      760                      765
Leu Lys Phe Gln Gly Gly Gln Ser Ser Ala Ala Thr Leu Leu Arg Arg
            770                      775                      780
Ser Lys Thr
785
```

```
        <210> 335
        <211> 194
        <212> PRT
        <213> Mouse

        <400> 335
Pro Gly Cys Lys Ser Cys Thr Val Cys Arg His Gly Leu Cys Arg Ser
```

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1011c2PCTSEQUENCE LISTING

```
1                  5                      10                  15
Val Glu Lys Asp Ser Val Val Cys Glu Cys His Pro Gly Trp Thr Gly
              20                  25                  30
Pro Leu Cys Asp Gln Glu Ala Arg Asp Pro Cys Leu Gly His Ser Cys
          35              40                  45
Arg His Gly Thr Cys Met Ala Thr Gly Asp Ser Tyr Val Cys Lys Cys
      50                  55                  60
Ala Glu Gly Tyr Gly Gly Ala Leu Cys Asp Gln Lys Asn Asp Ser Ala
65                      70                  75                  80
Ser Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
              85                  90                  95
Asp Arg Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly His
          100                 105                 110
His Cys Glu Gln Glu Asn Pro Cys Met Gly Glu Ile Val Arg Glu Ala
      115                 120                 125
Ile Arg Arg Gln Lys Asp Tyr Ala Ser Cys Ala Thr Ala Ser Lys Val
      130                 135                 140
Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Thr Thr Cys Cys Gln Pro
145                 150                 155                 160
Ile Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln Cys Thr Asp Gly Ser
              165                 170                 175
Ser Phe Val Glu Glu Val Glu Arg His Leu Glu Cys Gly Cys Arg Ala
          180                 185                 190
Cys Ser
```

```
        <210> 336
        <211> 274
        <212> PRT
        <213> Human

        <400> 336
Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu Pro Gly Ser Phe Arg
1                  5                      10                  15
Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro Asn Asn Arg Ser Cys
              20                  25                  30
Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro Cys Glu Gln Arg Cys
          35              40                  45
Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys His Gln Gly Tyr Glu
      50                  55                  60
Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile Asp Glu Cys Ser Tyr
65                  70                  75                  80
Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn Glu Pro Gly Arg Phe
              85                  90                  95
Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu Ala Thr Arg Leu Cys
          100                 105                 110
Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His Gln Cys Ser Glu Ala
      115                 120                 125
Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg Cys Val Asp Thr Asn
      130                 135                 140
Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu Asn Arg Cys Leu Cys
145                 150                 155                 160
Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro Ser Ser Ile Val His
              165                 170                 175
Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val Pro Ala Asp Val Phe
```

1011c2PCTSEQUENCE LISTING

```
              180                          185                        190
Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala Tyr Asn Ala Phe Gln
          195                        200                        205
Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr Ile Arg Gln Ile Asn
      210                        215                        220
Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro Val Thr Gly Pro Arg
225                        230                        235                        240
Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met Asn Ser Leu Met Ser
              245                        250                        255
Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val Phe Val Gly Ala Tyr
              260                        265                        270
Thr Phe
```

```
        <210> 337
        <211> 316
        <212> PRT
        <213> Mouse

        <400> 337
His Glu Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu Ala Tyr Asn
 1                5                       10                       15
Ile Asp Leu Gly Asp Ser Cys Ile Thr Val Gly Asn Thr Thr Thr His
              20                       25                       30
Val Met Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln
              35                       40                       45
Ala Ile Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala
       50                       55                       60
Lys Thr Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala
65                       70                       75                       80
Ser Gly Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys
                 85                       90                       95
Thr His Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg
              100                       105                       110
Asn Lys Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys
              115                       120                       125
Val Gln Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala
      130                       135                       140
Met Ser Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser
145                       150                       155                       160
Thr Thr Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln
              165                       170                       175
Leu Glu Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met
              180                       185                       190
Arg Gly Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp
          195                       200                       205
Ser Glu Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile
      210                       215                       220
Ser Gly Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys
225                       230                       235                       240
Arg Arg Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro
              245                       250                       255
Ser Ala Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp
              260                       265                       270
Leu Gly Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp
```

1011c2PCTSEQUENCE LISTING

```
             275                      280                      285
Glu Gln Phe Ala Ala Leu Ile Val Leu Gly Phe Ala Thr Leu Ser Ile
         290                      295                      300
Leu Phe Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys
305                      310                      315
```

```
         <210> 338
         <211> 237
         <212> PRT
         <213> Mouse

         <400> 338
Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
1                   5                   10                  15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
             20                  25                  30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
             35                  40                  45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
     50                  55                  60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
65                  70                  75                      80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
                 85                  90                  95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
             100                 105                 110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
         115                 120                 125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
     130                 135                 140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145                 150                 155                 160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
                 165                 170                 175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
             180                 185                 190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
         195                 200                 205
Lys Ser Leu Ala Ile Arg Thr Leu Gly Ser Pro Leu Ala Gly Ala Leu
210                 215                 220
His Ile Leu Leu Val Phe Leu Ile Ser Lys Leu Leu Phe
225                 230                 235
```

```
         <210> 339
         <211> 469
         <212> PRT
         <213> Mouse

         <400> 339
Met Leu Cys Leu Cys Leu Tyr Val Pro Ile Ala Gly Ala Ala Gln Thr
1                   5                   10                  15
Glu Phe Gln Tyr Phe Glu Ser Lys Gly Leu Pro Ala Glu Leu Lys Ser
             20                  25                  30
Ile Phe Lys Leu Ser Val Phe Ile Pro Ser Gln Glu Phe Ser Thr Tyr
         35                  40                  45
```

1011c2PCTSEQUENCE LISTING

```
Arg Gln Trp Lys Gln Lys Ile Val Gln Ala Gly Asp Lys Asp Leu Asp
    50              55                  60
Gly Gln Leu Asp Phe Glu Glu Phe Val His Tyr Leu Gln Asp His Glu
65              70                  75                  80
Lys Lys Leu Arg Leu Val Phe Lys Ser Leu Asp Lys Lys Asn Asp Gly
                85                  90                  95
Arg Ile Asp Ala Gln Glu Ile Met Gln Ser Leu Arg Asp Leu Gly Val
            100                 105                 110
Lys Ile Ser Glu Gln Gln Ala Glu Lys Ile Leu Lys Ser Met Asp Lys
        115                 120                 125
Asn Gly Thr Met Thr Ile Asp Trp Asn Glu Trp Arg Asp Tyr His Leu
    130                 135                 140
Leu His Pro Val Glu Asn Ile Pro Glu Ile Ile Leu Tyr Trp Lys His
145             150                 155                 160
Ser Thr Ile Phe Asp Val Gly Glu Asn Leu Thr Val Pro Asp Glu Phe
            165                 170                 175
Thr Val Glu Glu Arg Gln Thr Gly Met Trp Trp Arg His Leu Val Ala
        180                 185                 190
Gly Gly Gly Ala Gly Ala Val Ser Arg Thr Cys Thr Ala Pro Leu Asp
    195                 200                 205
Arg Leu Lys Val Leu Met Gln Val His Ala Ser Arg Ser Asn Asn Met
    210                 215                 220
Cys Ile Val Gly Gly Phe Thr Gln Met Ile Arg Glu Gly Gly Ala Lys
225             230                 235                 240
Ser Leu Trp Arg Gly Asn Gly Ile Asn Val Leu Lys Ile Ala Pro Glu
                245                 250                 255
Ser Ala Ile Lys Phe Met Ala Tyr Glu Gln Met Lys Arg Leu Val Gly
            260                 265                 270
Ser Asp Gln Glu Thr Leu Arg Ile His Glu Arg Leu Val Ala Gly Ser
        275                 280                 285
Leu Ala Gly Ala Ile Ala Gln Ser Ser Ile Tyr Pro Met Glu Val Leu
    290                 295                 300
Lys Thr Arg Met Ala Leu Arg Lys Thr Gly Gln Tyr Ser Gly Met Leu
305             310                 315                 320
Asp Cys Ala Arg Arg Ile Leu Ala Lys Glu Gly Val Ala Ala Phe Tyr
                325                 330                 335
Lys Gly Tyr Ile Pro Asn Met Leu Gly Ile Ile Pro Tyr Ala Gly Ile
            340                 345                 350
Asp Leu Ala Val Tyr Glu Thr Leu Lys Asn Thr Trp Leu Gln Arg Tyr
        355                 360                 365
Ala Val Asn Ser Ala Asp Pro Gly Val Phe Val Leu Leu Ala Cys Gly
    370                 375                 380
Thr Ile Ser Ser Thr Cys Gly Gln Leu Ala Ser Tyr Pro Leu Ala Leu
385             390                 395                 400
Val Arg Thr Arg Met Gln Ala Gln Ala Ser Ile Glu Gly Ala Pro Glu
            405                 410                 415
Val Thr Met Ser Ser Leu Phe Lys Gln Ile Leu Arg Thr Glu Gly Ala
            420                 425                 430
Phe Gly Leu Tyr Arg Gly Leu Ala Pro Asn Phe Met Lys Val Ile Pro
        435                 440                 445
Ala Val Ser Ile Ser Tyr Val Val Tyr Glu Asn Leu Lys Ile Thr Leu
    450             455                 460
Gly Val Gln Ser Arg
465
```

1011c2PCTSEQUENCE LISTING

```
<210> 340
<211> 99
<212> PRT
<213> Mouse

<400> 340
Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
1               5               10              15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
        20              25              30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
        35              40              45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
        50              55              60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
65              70              75              80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
                85              90              95
Tyr Glu Glu
```

```
<210> 341
<211> 431
<212> PRT
<213> Mouse

<400> 341
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Thr Leu Pro Ser
1               5               10              15
Leu Gly Ala Gly Gly Glu Ser Pro Glu Ala Pro Pro Gln Ser Trp Thr
        20              25              30
Gln Leu Trp Leu Phe Arg Phe Leu Leu Asn Val Ala Gly Tyr Ala Ser
        35              40              45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Leu Arg Arg Lys Asn
        50              55              60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65              70              75              80
Val Phe Gly Asn Glu Pro Lys Ala Pro Asp Glu Val Leu Leu Ala Pro
                85              90              95
Arg Thr Glu Thr Ala Glu Ser Thr Pro Ser Trp Gln Val Leu Lys Leu
                100             105             110
Val Phe Cys Ala Ser Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Ile
        115             120             125
Leu Gln Glu Arg Val Met Thr Gly Ser Tyr Gly Ala Thr Ala Thr Ser
        130             135             140
Pro Gly Glu His Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145             150             155             160
Val Leu Ala Leu Val Val Ala Gly Leu Tyr Cys Val Leu Arg Lys Gln
                165             170             175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
        180             185             190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
        195             200             205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
210             215             220
```

1011c2PCTSEQUENCE LISTING

```
Met Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225             230             235                 240
Leu Thr Ala Gly Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
            245             250                 255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
        260             265                 270
Val Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
        275             280                 285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
    290             295                 300
Gly Val Asn Leu Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305             310             315                 320
Gln Gly Ala Leu Leu Glu Gly Ala Arg Phe Met Gly Arg His Ser Glu
            325             330                 335
Phe Ala Leu His Ala Leu Leu Leu Ser Ile Cys Ser Ala Phe Gly Gln
            340             345                 350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
            355             360                 365
Ile Ile Met Thr Leu Arg Gln Ala Ile Ala Ile Leu Leu Ser Cys Leu
370             375             380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385             390             395                 400
Val Phe Thr Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Lys Gln
            405             410                 415
Arg Gly Lys Lys Ala Val Pro Thr Glu Pro Pro Val Gln Lys Val
            420             425                 430
```

```
<210> 342
<211> 51
<212> PRT
<213> Mouse

<400> 342
Leu Lys Phe Ser His Pro Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
1               5               10                  15
Asn Gly Ala Cys Ala Phe His His Glu Leu Lys Gln Ala Ile Cys Arg
            20              25                  30
Cys Phe Thr Gly Tyr Thr Gly Gln Arg Cys Glu His Leu Thr Leu Thr
        35              40                  45
Ser Tyr Ala
    50
```

```
<210> 343
<211> 51
<212> PRT
<213> Human
<400> 343
Leu Lys Phe Ser His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile
1               5               10                  15
Asn Gly Ala Cys Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg
            20              25                  30
Cys Phe Thr Gly Tyr Thr Gly Glu Arg Cys Glu His Leu Thr Leu Thr
        35              40                  45
Ser Tyr Ala
    50
```

1011c2PCTSEQUENCE LISTING

```
        <210> 344
        <211> 95
        <212> PRT
        <213> Human

        <400> 344
Ala Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala Arg Val
1               5                   10                  15
Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr
            20                  25                  30
Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu
        35                  40                  45
Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly
    50                  55                  60
Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile
65                  70                  75                  80
Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
                85                  90                  95

        <210> 345
        <211> 77
        <212> PRT
        <213> Mouse

        <400> 345
Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
1               5                   10                  15
Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
            20                  25                  30
Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu
        35                  40                  45
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
        50                  55                  60
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
65                  70                  75

        <210> 346
        <211> 77
        <212> PRT
        <213> Human

        <400> 346
Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
1               5                   10                  15
Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
            20                  25                  30
Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu
        35                  40                  45
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
        50                  55                  60
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
65                  70                  75

        <210> 347
```

1011c2PCTSEQUENCE LISTING

```
<211> 215
<212> PRT
<213> Mouse

<400> 347
Met Leu Ser Leu Arg Ser Leu Leu Pro His Leu Gly Leu Phe Leu Cys
1               5                   10                  15
Leu Ala Leu His Leu Ser Pro Ser Leu Ser Ala Ser Asp Asn Gly Ser
            20                  25                  30
Cys Val Val Leu Asp Asn Ile Tyr Thr Ser Asp Ile Leu Glu Ile Ser
        35                  40                  45
Thr Met Ala Asn Val Ser Gly Gly Asp Val Thr Tyr Thr Val Thr Val
    50                  55                  60
Pro Val Asn Asp Ser Val Ser Ala Val Ile Leu Lys Ala Val Lys Glu
65                  70                  75                  80
Asp Asp Ser Pro Val Gly Thr Trp Ser Gly Thr Tyr Glu Lys Cys Asn
                85                  90                  95
Asp Ser Ser Val Tyr Tyr Asn Leu Thr Ser Gln Ser Gln Ser Val Phe
                100                 105                 110
Gln Thr Asn Trp Thr Val Pro Thr Ser Glu Asp Val Thr Lys Val Asn
                115                 120                 125
Leu Gln Val Leu Ile Val Val Asn Arg Thr Ala Ser Lys Ser Ser Val
    130                 135                 140
Lys Met Glu Gln Val Gln Pro Ser Ala Ser Thr Pro Ile Pro Glu Ser
145                 150                 155                 160
Ser Glu Thr Ser Gln Thr Ile Asn Thr Thr Pro Thr Val Asn Thr Ala
                165                 170                 175
Lys Thr Thr Ala Lys Asp Thr Ala Asn Thr Thr Ala Val Thr Thr Ala
                180                 185                 190
Asn Thr Thr Ala Asn Thr Thr Ala Val Thr Thr Ala Lys Thr Thr Ala
        195                 200                 205
Lys Ser Leu Ala Ile Arg Thr
210                 215

<210> 348
<211> 21
<212> PRT
<213> Mouse

<400> 348
Gly Tyr Ser Asp Gly Tyr Gln Val Cys Ser Arg Phe Gly Ser Lys Val
1               5                   10                  15
Pro Gln Phe Leu Asn

<210> 349
<211> 417
<212> DNA
<213> Mouse

<400> 349
gctagccgtg cacccagctc tccggagcgc gtgcaggcga gccgagcgcc ccgtccgcgg
        60
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1011c2PCTSEQUENCE LISTING

180
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417

&lt;210&gt; 350
&lt;211&gt; 1837
&lt;212&gt; DNA
&lt;213&gt; Mouse

&lt;400&gt; 350
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480
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1080
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1140
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1011c2PCTSEQUENCE LISTING
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                1260
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                1320
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                1380
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                1740
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                1800
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              1837


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        <212> DNA
        <213> Mouse


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         180
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         360
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         420
ggacatccaa ggcctgccta aaaggcaagc aggcctgggg agcagtcgcc cagaagcccc
         480
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         540
caagttcctc aatgacacgg aggagctagc tgtggccagg ccagaggaca ctgtgggtac
         600
cctaaaaagg tgagtaggcc ggagagaggc cagttgctcg tgacttgttc ctcagatgat
         660
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1011c2PCTSEQUENCE LISTING

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840
aatgaagttg atctaccagg gtcggctgct gcaggaccca gcacgcacac tgagttccct
900
gaacattacc aacaactgcg tgatccactg ccaccgctca c
941

```
<210> 352
<211> 571
<212> DNA
<213> Mouse
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<400> 352
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120
atttggatgt cttttggttc cgtgaacaag tagaaattgc atgtgtctac cggtgacagt
180
gtggtgtcac tgggccctgt gggtggctca cttacctctg attccgtctg tgggaaagtc
240
ccagtgtacc caaatgtggc attgttgcat gccttgggtg tgtgtgggag attgtctctg
300
tctctcagac cctttgtggc tttgtctgtt gaaagagaca gagacccctt gtggttttct
360
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420
cccctcctca tgctgaccct tcaatatctg gcagtgcatt gttcccaagc cccccttgtc
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tatgggaatg tcagggctct ctcaccttga cagctgataa ttccattcct cgactcttga
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571

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<210> 353
<211> 467
<212> DNA
<213> Rat
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<400> 353
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catggtgcgc caggccccga aggcaccgcg cccgaccccg cccactacag ggagcgagtc
180
aaggccatgt tctaccacgc ctacgacagt tacctggaaa atgcctttcc ctacgatgag
240
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300
gatgccctgg acaccttgct gattttgggg aatacctctg aattccaaag agtggtggag
360
gttctccagg acaaacgtgg actttgatat cgacgtcaat gcctctgtgt tcgaaaccaa
420

1011c2PCTSEQUENCE LISTING
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        <210> 354
        <211> 528
        <212> DNA
        <213> Rat

        <400> 354
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      120
tctcgagttg ccactcccaa gccagccccc actggccata tggcatcata tctgggggtc
      180
aggagggcct gtgcaggctt tggacagcca cttgccacag cagaggagag agtgaggttt
      240
ccaggagcag caggaaggaa gaccccagaa ttccccaggg ctctttgagt ggtaatgttg
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acttctggag agtctgccca ccttgtgctc acacaagcat ggacaggaca ctgggacttt
      360
tatcctgttg ttaagctgtt tccacagaag cccgttcagg tagttacttc acccacattg
      420
gccctatagc cagaggagtg ccctggctaa ctgcagtgtg agcttgtaag caacagaagt
      480
gcccaggagc tgaccccaaa ggccaggaag gctcgagctt gccacttt
      528

        <210> 355
        <211> 473
        <212> DNA
        <213> Mouse

        <400> 355
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      60
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      120
ggcatttgtt gcgtctttcc tcctgtggcc ttcagcactg ataagaatct attattggta
      180
ctggcggagg acactgggca tgcaagttcg ctacgcacac catgaggact atcagttctg
      240
ttactccttc cggggcaggc caggacacaa gccatccatc cttatgctcc atggattctc
      300
cgcacacaag gacatgtggc tcagcgtggt caagttcctt ccgaagaacc tgcacttggt
      360
ctgtgtggac atgcctgggc atgaaggcac cacccgctcc tccctggatg acctgtccat
      420
agtggggcaa gttaaaagga tacatcagtt tgtagaatgc cttaagctga aca
      473

        <210> 356
        <211> 431
        <212> DNA
        <213> Rat

1011c2PCTSEQUENCE LISTING

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120
ggcttcggct gggctaacgc gcgagtgtgg tgggactatc ctaggaggtg ttcctggaga
180
gagaggcgat ggcgtcaagt agtaactggc tgtccggagt gaatgtcgtt cttgtgatgg
240
cgtacgggag cctggtattc gtattgctgt ttatttttgt gaagagacaa atcatgcgct
300
ttgcaatgaa atctagaagg ggacctcatg tccctgtggg acacaatgcc ccgaaggact
360
taaaagagga aattgatatt cggctatcca gagttcagga catcaagtat gaaccgcagc
420
tccttgcaga t
431


&lt;210&gt; 357
&lt;211&gt; 1206
&lt;212&gt; DNA
&lt;213&gt; Mouse

&lt;400&gt; 357

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acagtgggat ccgtgggcgc cgtgatgggc tccgaggatt ctgtgcccgg tggcgtgtgc
120
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480
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600
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720
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780
gtgtgagctg cagccactgg gcctggcatt tgacgccatc ccgattttat ttattgttat
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agaaaatatt ctaatttatg tcacatggac atttcccaaa cctggcctgg aaccacttgg
900

1011c2PCTSEQUENCE LISTING
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  1020
agggatggca gctgcatgga gatccccctg ctatgatctc cccacctgct ttctaggctg
  1080
gagctgtcgc agggcacagc cgatgagttg gtgtttgcat atggctggcc tcagaccaga
  1140
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  1200
aacctg
  1206
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        <210> 358
        <211> 1052
        <212> DNA
        <213> Rat

        <400> 358
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  120
gacttccaga agggtggtcc tcaactggtg tgcagtctgc ctggtcccca aggccacctg
  180
gccctccagg agcaccagga tcctcaggaa tggtgggaag aatgggtttt cctggtaagg
  240
atggccaaga cggccaggac ggagaccgag gggacagtgg agaagaaggt ccacctggca
  300
ggacaggcaa ccgaggaaaa caaggaccaa agggcaaagc tggggccatt gggagagcgg
  360
gtcctcgagg acccaagggg gtcagtggta cccccgggaa acatggtata ccgggcaaga
  420
agggacctaa gggcaagaaa ggggaacctg gctcccagg cccctgtagc tgcggcagta
  480
gccgagccaa gtcggccttt tcggtggcgg taaccaagag ttacccacgt gagcgactgc
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  600
agttcgtctg cagcgtgcca gggatctatt actttaccta tgacattacg ctggccaaca
  660
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  720
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  780
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  900
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  960
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  1020
gcctcctctg gtgctgcttt aaaaaaaaaa aa
  1052
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1011c2PCTSEQUENCE LISTING

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        <211> 1134
        <212> DNA
        <213> Rat

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   180
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   240
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   420
cctgtctgtg gtaggggccc tcttactcta catggccttc ctgatgctgg tggaccctct
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   720
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   960
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   1020
gccgtcaata gctcggtggg tgcgacgaaa gtgtgaccca gccctcagcc tgtgctctac
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        <210> 360
        <211> 876
        <212> DNA
        <213> Mouse

        <400> 360
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   60
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1011c2PCTSEQUENCE LISTING
120
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180
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240
aaccgcatct cccgaatccc cgtctccttc tgccgcctca ggcacctgca ggtcgttctg
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360
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660
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720
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780
cgagaggagc ctgcagggga ggagaggcgg cgcccagaca ctttgcagtt gtggcaggaa
840
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876

        <210> 361
        <211> 495
        <212> DNA
        <213> Mouse

        <400> 361
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ggacagaggc ccctctgttc cccagggcct gctgaaggca gcgagaagca gcggccaact
120
caacttggcg ggaaggaacc tcggggaagt ccctcagtgt gtttggagaa taaatgtgga
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240
gacagatctg accaaactca tcatctccag caataaactt cagtctctct ctgatgacct
300
ccgactcttg cctgccctta ctgttcttga tatacatgat aatcagctga catctcttcc
360
ttcagctata agagagctag acaatcttca gaaacttaat gtcagccata caaaactgaa
420
aatactgcct gaagaaatta caagcttaaa aaacctgagg acgctgcacc tccagcacaa
480
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495

        <210> 362
        <211> 349

1011c2PCTSEQUENCE LISTING

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&lt;213&gt; Mouse

&lt;400&gt; 362
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    120
atggaaccca gggctttgtt taggcctgac aaggctctgc ccctgagctg tgccaagccc
    180
acctccctct gtgtacaaag ctcctttctt gggtgaccaa catcttcctg tctttgagca
    240
accaaggcca gatgcgagcc acccagaagt taattaaacc aggttcatcg ggagtttgct
    300
gaaatgttaa gcatactctg ttctagagag ggagtgaaga aaggggcca
    349

&lt;210&gt; 363
&lt;211&gt; 380
&lt;212&gt; DNA
&lt;213&gt; Mouse

&lt;400&gt; 363
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gacaaggtga agctgacctg gagggaccga ttcccagcct atttcaccaa tcttgtctcc
    120
atcatcttca tgatcgcagt gacatttgca atcgtcctcg gagttatcat ctatagaatc
    180
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    240
acagtcacgg ccaccgctgt tatcatcaac ctcgtggtca tcattctgct ggatgaagtt
    300
tacggctgca ttgccaggtg gctcaccaag attggtgagt gccatgtgca ggacagcata
    360
ggcagcatgg gcctagggca
    380

&lt;210&gt; 364
&lt;211&gt; 351
&lt;212&gt; DNA
&lt;213&gt; Mouse

&lt;400&gt; 364
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ttcgaccgcg tgaagatggg ctttgtcatg ggttgcgccg tgggtatggc ggccggggcc
    120
ctgttcggca ccttctcctg tctcaggatc ggaatgcggg gtcgggagct gatgggcggc
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    240
ggcatacgat gctaattagg gcacggatgc cctgctacac ccaaacttcc tcatccattt
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351

        <210> 365
        <211> 854
        <212> DNA
        <213> Rat

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Leu Ala Leu His Pro Glu Val Pro Gly Leu Tyr Asn Tyr Leu Pro Trp
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Met Leu Val


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Thr Met Gly Lys Ile Ala Val Ala Ser Lys Leu Met Trp Cys Ser Ala
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Ala Val Asp Ile Leu Phe Leu Leu Asp Gly Ser His Ser Ile Gly Lys
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Gly Ser Phe Glu Arg Ser Lys Arg Phe Ala Ile Ala Ala Cys Asp Ala
65                  70                  75                  80
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Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Arg Gln
                100                 105                 110
Glu Val Lys Glu Ser Ile Lys Gly Ile Val Phe Lys Gly Gly Arg Thr
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Glu Thr Gly Leu Ala Leu Lys Arg Leu Ser Arg Gly Phe Pro Gly Gly
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Leu Thr Leu Ala Ser Glu Pro Lys Asp Arg His Val Leu Leu Ala Glu
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Gln Val Glu Asp Ala Thr Asn Gly Leu Leu Ser Thr Leu Ser Ser Ser
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225                       230                   235                   240
Cys Glu Arg Arg Thr Leu Glu Thr Val Arg Glu Leu Ala Gly Asn Ala
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Leu Cys Trp Arg Gly Ser Arg Gln Ala Asp Thr Val Leu Ala Leu Pro
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Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Gln Thr His Pro Ala Asn
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Cys Tyr Arg Thr Ile Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys Gln
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Asn Gly Gly Thr Cys Ile Pro Glu Gly Val Asp Arg Tyr His Cys Leu
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Cys Pro Leu Ala Phe Gly Gly Glu Val Asn Cys Ala Pro Lys Leu Ser
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        <400>  375
Met Glu Leu Ser Asp Val Thr Leu Ile Glu Gly Val Gly Asn Glu Val
1                   5                         10                        15
Met Val Val Ala Gly Val Val Ala Leu Thr Leu Ala Leu Val Leu Ala
            20                        25                    30
Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Asn Asn Gln Leu Leu Gly
            35                        40                    45
Thr Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val
    50                        55                    60
Asp Gln Leu Val Asn Gln Gly Thr Pro Glu Pro Thr Glu His Pro His
65                        70                    75                    80
Pro Ser Gly Gly Asn Asp Asp Lys Ala Glu Glu Thr Ser Asp Ser Gly
                85                        90                    95
Gly Asp Ala Thr Gly Glu Pro Gly Ala Arg Gly Glu Met Glu Pro Ser
                100                       105                   110
Leu Glu His Leu Leu Asp Ile Gln Gly Leu Pro Lys Arg Gln Ala Gly
```

1011c2PCTSEQUENCE LISTING

```
            115                    120                      125
Leu Gly Ser Ser Arg Pro Glu Ala Pro Leu Gly Leu Asp Asp Gly Ser
        130                    135                  140
Cys Leu Ser Pro Ser Pro Ser Leu Ile Asn Val Arg Leu Lys Phe Leu
145                    150                  155                  160
Asn Asp Thr Glu Glu Leu Ala Val Ala Arg Pro Glu Asp Thr Val Gly
                   165                  170                  175
Thr Leu Lys Arg
            180
```

```
        <210> 376
        <211> 68
        <212> PRT
        <213> Mouse
```

```
        <400> 376
Met Cys Leu Pro Val Thr Val Trp Cys His Trp Ala Leu Trp Val Ala
1                5                  10                   15
His Leu Pro Leu Ile Pro Ser Val Gly Lys Ser Gln Cys Thr Gln Met
            20                  25                   30
Trp His Cys Cys Met Pro Trp Val Cys Val Gly Asp Cys Leu Cys Leu
        35                  40                  45
Ser Asp Pro Leu Trp Leu Cys Leu Leu Lys Glu Thr Glu Thr Pro Cys
    50                  55                  60
Gly Phe Leu Ser
65
```

```
        <210> 377
        <211> 107
        <212> PRT
        <213> Rat
```

```
        <400> 377
Met Pro Phe Arg Leu Leu Ile Pro Leu Gly Leu Val Cys Val Leu Leu
1                5                  10                   15
Pro Leu His His Gly Ala Pro Gly Pro Glu Gly Thr Ala Pro Asp Pro
            20                  25                   30
Ala His Tyr Arg Glu Arg Val Lys Ala Met Phe Tyr His Ala Tyr Asp
        35                  40                  45
Ser Tyr Leu Glu Asn Ala Phe Pro Tyr Asp Glu Leu Arg Pro Leu Thr
    50                  55                  60
Cys Asp Gly His Asp Thr Trp Gly Ser Phe Ser Leu Thr Leu Ile Asp
65                  70                  75                  80
Ala Leu Asp Thr Leu Leu Ile Leu Gly Asn Thr Ser Glu Phe Gln Arg
                85                  90                  95
Val Val Glu Val Leu Gln Asp Lys Arg Gly Leu
            100                  105
```

```
        <210> 378
        <211> 95
        <212> PRT
        <213> Rat
```

```
        <400> 378
Met Trp Phe Leu Pro Cys Ser Val Pro Leu Val Ile Ser Ser Cys His
```

1011c2PCTSEQUENCE LISTING

```
1                   5                        10                      15
Ser Gln Ala Ser Pro His Trp Pro Tyr Gly Ile Ile Ser Gly Gly Gln
                20                        25                      30
Glu Gly Leu Cys Arg Leu Trp Thr Ala Thr Cys His Ser Arg Gly Glu
         ·35                       40                      45
Ser Glu Val Ser Arg Ser Ser Arg Lys Glu Asp Pro Arg Ile Pro Gln
         50                       55                      60
Gly Ser Leu Ser Gly Asn Val Asp Phe Trp Arg Val Cys Pro Pro Cys
65                       70                      75                      80
Ala His Thr Ser Met Asp Arg Thr Leu Gly Leu Leu Ser Cys Cys
                85                       90                      95
```

        <210> 379
        <211> 138
        <212> PRT
        <213> Mouse

        <400> 379
```
Met Asp Leu Asp Val Val Asn Met Phe Val Ile Ala Gly Gly Thr Leu
1                   5                        10                      15
Ala Ile Pro Ile Leu Ala Phe Val Ala Ser Phe Leu Leu Trp Pro Ser
                20                        25                      30
Ala Leu Ile Arg Ile Tyr Tyr Trp Tyr Trp Arg Arg Thr Leu Gly Met
         35                       40                      45
Gln Val Arg Tyr Ala His His Glu Asp Tyr Gln Phe Cys Tyr Ser Phe
         50                       55                      60
Arg Gly Arg Pro Gly His Lys Pro Ser Ile Leu Met Leu His Gly Phe
65                       70                      75                      80
Ser Ala His Lys Asp Met Trp Leu Ser Val Val Lys Phe Leu Pro Lys
                85                       90                      95
Asn Leu His Leu Val Cys Val Asp Met Pro Gly His Glu Gly Thr Thr
                100                       105                      110
Arg Ser Ser Leu Asp Asp Leu Ser Ile Val Gly Gln Val Lys Arg Ile
         115                       120                      125
His Gln Phe Val Glu Cys Leu Lys Leu Asn
         130                       135
```

        <210> 380
        <211> 81
        <212> PRT
        <213> Rat

        <400> 380
```
Met Ala Ser Ser Ser Asn Trp Leu Ser Gly Val Asn Val Val Leu Val
1                   5                        10                      15
Met Ala Tyr Gly Ser Leu Val Phe Val Leu Leu Phe Ile Phe Val Lys
                20                        25                      30
Arg Gln Ile Met Arg Phe Ala Met Lys Ser Arg Arg Gly Pro His Val
         35                       40                      45
Pro Val Gly His Asn Ala Pro Lys Asp Leu Lys Glu Glu Ile Asp Ile
         50                       55                      60
Arg Leu Ser Arg Val Gln Asp Ile Lys Tyr Glu Pro Gln Leu Leu Ala
65                       70                      75                      80
Asp
```

1011c2PCTSEQUENCE LISTING

```
        <210> 381
        <211> 257
        <212> PRT
        <213> Mouse

        <400> 381
Met Arg Ser Gly Ala Leu Trp Pro Leu Leu Trp Gly Ala Leu Val Trp
1               5                   10                  15
Thr Val Gly Ser Val Gly Ala Val Met Gly Ser Glu Asp Ser Val Pro
                20                  25                  30
Gly Gly Val Cys Trp Leu Gln Gln Gly Arg Glu Ala Thr Cys Ser Leu
            35                  40                  45
Val Leu Lys Thr Arg Val Ser Arg Glu Glu Cys Cys Ala Ser Gly Asn
        50                  55                  60
Ile Asn Thr Ala Trp Ser Asn Phe Thr His Pro Gly Asn Lys Ile Ser
65                  70                  75                  80
Leu Leu Gly Phe Leu Gly Leu Val His Cys Leu Pro Cys Lys Asp Ser
                85                  90                  95
Cys Asp Gly Val Glu Cys Gly Pro Gly Lys Ala Cys Arg Met Leu Gly
                100                 105                 110
Gly Arg Pro Thr Leu Arg Ser Cys Val Pro Asn Cys Glu Gly Leu Pro
            115                 120                 125
Ala Gly Phe Gln Val Cys Gly Ser Asp Gly Ala Thr Tyr Arg Asp Glu
            130                 135                 140
Cys Glu Leu Arg Thr Ala Arg Cys Arg Gly His Pro Asp Leu Arg Val
145                 150                 155                 160
Met Tyr Arg Gly Arg Cys Gln Lys Ser Cys Ala Gln Val Val Cys Pro
                165                 170                 175
Arg Pro Gln Ser Cys Leu Val Asp Gln Thr Gly Ser Ala His Cys Val
                180                 185                 190
Val Cys Arg Ala Ala Pro Cys Pro Val Pro Ser Asn Pro Gly Gln Glu
            195                 200                 205
Leu Cys Gly Asn Asn Asn Val Thr Tyr Ile Ser Ser Cys His Leu Arg
            210                 215                 220
Gln Ala Thr Cys Phe Leu Gly Arg Ser Ile Gly Val Arg His Pro Gly
225                 230                 235                 240
Ile Cys Thr Gly Gly Pro Lys Val Pro Ala Glu Glu Glu Glu Asn Phe
                245                 250                 255
Val


        <210> 382
        <211> 285
        <212> PRT
        <213> Rat

        <400> 382
Met Ile Ser Trp Met Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
1               5                   10                  15
Pro Met Leu Gly Ala Phe Ala Arg Arg Asp Phe Gln Lys Gly Gly Pro
                20                  25                  30
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
            35                  40                  45
Gly Ala Pro Gly Ser Ser Gly Met Val Gly Arg Met Gly Phe Pro Gly
```

1011c2PCTSEQUENCE LISTING

```
          50                      55                      60
Lys Asp Gly Gln Asp Gly Gln Asp Gly Asp Arg Gly Asp Ser Gly Glu
65                      70                      75                      80
Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Gln Gly Pro Lys
                    85                      90                      95
Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly
                100                     105                     110
Val Ser Gly Thr Pro Gly Lys His Gly Ile Pro Gly Lys Lys Gly Pro
        115                     120                     125
Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly
    130                     135                     140
Ser Ser Arg Ala Lys Ser Ala Phe Ser Val Ser Val Thr Lys Ser Tyr
145                     150                     155                     160
Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu
                165                     170                     175
Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Ser Val Pro
                180                     185                     190
Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu
                195                     200                     205
Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp
    210                     215                     220
Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala
225                     230                     235                     240
Leu Lys Glu Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln
                245                     250                     255
Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly
                260                     265                     270
Phe Leu Ile Tyr Ala Asp Gln Gly Asp Pro Asn Glu Val
        275                     280                     285
```

```
    <210> 383
    <211> 183
    <212> PRT
    <213> Rat

    <400> 383
Met Lys Leu Leu Cys Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
1                   5                       10                      15
Pro Ala Gln Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
                20                      25                      30
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
        35                      40                      45
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
        50                      55                      60
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65                      70                      75                      80
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
                85                      90                      95
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
                100                     105                     110
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
        115                     120                     125
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
        130                     135                     140
Ile Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
```

1011c2PCTSEQUENCE LISTING

```
145                    150                    155                         160
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
                165                    170                    175
Asp Arg His Lys Met Leu Ser
                180
```

```
        <210> 384
        <211> 292
        <212> PRT
        <213> Mouse


        <400> 384
Cys Gln Leu Pro Leu Arg Val Leu Ile Ile Ser Asn Asn Lys Leu Gly
  1             5                   10                  15
Ala Leu Pro Pro Asp Ile Ser Thr Leu Gly Ser Leu Arg Gln Leu Asp
                20                  25                  30
Val Ser Ser Asn Glu Leu Gln Ser Leu Pro Val Glu Leu Cys Ser Leu
                35                  40                  45
Arg Ser Leu Arg Asp Leu Asn Val Arg Arg Asn Gln Leu Ser Thr Leu
      50                  55                  60
Pro Asp Glu Leu Gly Asp Leu Pro Leu Val Arg Leu Asp Phe Ser Cys
65                  70                  75                  80
Asn Arg Ile Ser Arg Ile Pro Val Ser Phe Cys Arg Leu Arg His Leu
                85                  90                  95
Gln Val Val Leu Leu Asp Ser Asn Pro Leu Gln Ser Pro Pro Ala Gln
                100                 105                 110
Ile Cys Leu Lys Gly Lys Leu His Ile Phe Lys Tyr Leu Thr Met Glu
                115                 120                 125
Ala Gly Arg Arg Gly Ala Ala Leu Gly Asp Leu Val Pro Ser Arg Pro
      130                 135                 140
Pro Ser Phe Ser Pro Cys Pro Ala Glu Asp Leu Phe Pro Gly Arg Arg
145                 150                 155                 160
Tyr Asp Gly Gly Leu Asp Ser Gly Phe His Ser Val Asp Ser Gly Ser
                165                 170                 175
Lys Arg Trp Ser Gly Asn Glu Ser Thr Asp Asp Phe Ser Glu Leu Ser
                180                 185                 190
Phe Arg Ile Ser Glu Leu Ala Arg Asp Pro Arg Gly Pro Arg Gln Pro
                195                 200                 205
Arg Glu Asp Gly Ala Gly Asp Gly Asp Leu Glu Gln Ile Asp Phe Ile
      210                 215                 220
Asp Ser His Val Pro Gly Glu Asp Glu Asp Arg Ser Ala Ala Glu Glu
225                 230                 235                 240
Gln Leu Pro Ser Glu Leu Ser Leu Val Ala Gly Asp Val Glu Lys Pro
                245                 250                 255
Ser Ser Ser Arg Arg Glu Glu Pro Ala Gly Glu Glu Arg Arg Arg Pro
                260                 265                 270
Asp Thr Leu Gln Leu Trp Gln Glu Arg Glu Arg Lys Gln Gln Gln Gln
      275                 280                 285
Ser Gly Gly Trp
      290


        <210> 385
        <211> 164
        <212> PRT
        <213> Mouse
```

1011c2PCTSEQUENCE LISTING

```
        <400> 385
Ser Arg Gln Leu Arg Ala Pro Arg Phe Asp Pro Arg Ala Gly Phe His
1               5               10              15
Ala Glu Gly Lys Asp Arg Gly Pro Ser Val Pro Gln Gly Leu Leu Lys
            20              25              30
Ala Ala Arg Ser Ser Gly Gln Leu Asn Leu Ala Gly Arg Asn Leu Gly
        35              40              45
Glu Val Pro Gln Cys Val Trp Arg Ile Asn Val Asp Ile Pro Glu Glu
    50              55              60
Ala Asn Gln Asn Leu Ser Phe Ser Ser Thr Glu Arg Trp Trp Asp Gln
65              70              75              80
Thr Asp Leu Thr Lys Leu Ile Ile Ser Ser Asn Lys Leu Gln Ser Leu
            85              90              95
Ser Asp Asp Leu Arg Leu Leu Pro Ala Leu Thr Val Leu Asp Ile His
        100             105             110
Asp Asn Gln Leu Thr Ser Leu Pro Ser Ala Ile Arg Glu Leu Asp Asn
        115             120             125
Leu Gln Lys Leu Asn Val Ser His Asn Lys Leu Lys Ile Leu Pro Glu
    130             135             140
Glu Ile Thr Ser Leu Lys Asn Leu Arg Thr Leu His Leu Gln His Asn
145             150             155             160
Glu Leu Thr Cys
```

```
        <210> 386
        <211> 71
        <212> PRT
        <213> Mouse
```

```
        <400> 386
Ser Leu Ser Ile Leu Pro Ala Val Arg Val Ser Pro Arg Pro Thr Tyr
1               5               10              15
Pro Ser Thr Ala Ser Ser Met Ala Ala Phe Leu Val Thr Gly Phe Phe
            20              25              30
Phe Ser Leu Phe Val Val Leu Gly Met Glu Pro Arg Ala Leu Phe Arg
        35              40              45
Pro Asp Lys Ala Leu Pro Leu Ser Cys Ala Lys Pro Thr Ser Leu Cys
    50              55              60
Val Gln Ser Ser Phe Leu Gly
65              70
```

```
        <210> 387
        <211> 126
        <212> PRT
        <213> Mouse
```

```
        <400> 387
Glu Tyr Glu Ala Arg Val Leu Glu Lys Ser Leu Arg Lys Glu Ser Arg
1               5               10              15
Asn Lys Glu Thr Asp Lys Val Lys Leu Thr Trp Arg Asp Arg Phe Pro
            20              25              30
Ala Tyr Phe Thr Asn Leu Val Ser Ile Ile Phe Met Ile Ala Val Thr
        35              40              45
Phe Ala Ile Val Leu Gly Val Ile Ile Tyr Arg Ile Ser Thr Ala Ala
```

1011c2PCTSEQUENCE LISTING
```
            50                    55                    60
Ala Leu Ala Met Asn Ser Ser Pro Ser Val Arg Ser Asn Ile Arg Val
65                    70                    75                    80
Thr Val Thr Ala Thr Ala Val Ile Ile Asn Leu Val Val Ile Ile Leu
                      85                    90                    95
Leu Asp Glu Val Tyr Gly Cys Ile Ala Arg Trp Leu Thr Lys Ile Gly
                100                   105                   110
Glu Cys His Val Gln Asp Ser Ile Gly Ser Met Gly Leu Gly
            115                   120                   125
```

        <210> 388
        <211> 84
        <212> PRT
        <213> Rat


        <400> 388
```
Ala Ala Glu Asn Glu Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser
1               5                   10                  15
Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly Phe Val Met Gly Cys
            20                  25                  30
Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu
        35                  40                  45
Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr
    50                  55                  60
Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met
65                  70                  75                  80
Gly Ile Arg Cys
```

        <210> 389
        <211> 284
        <212> PRT
        <213> Rat


        <400> 389
```
Gly Gly Ser Ser Val Ser His Val Leu Arg Gly Ser Gly Gln Glu Arg
1               5                   10                  15
Ser Pro Pro Pro Ala Ser Met Gln Pro Pro Trp Gly Leu Ala Leu Pro
            20                  25                  30
Leu Leu Leu Pro Trp Val Ala Gly Gly Val Gly Thr Ser Pro Arg Asp
        35                  40                  45
Tyr Trp Leu Pro Ala Leu Ala His Gln Pro Gly Val Cys His Tyr Gly
    50                  55                  60
Thr Lys Thr Ala Cys Cys Tyr Gly Trp Lys Arg Asn Ser Lys Gly Val
65                  70                  75                  80
Cys Glu Ala Val Cys Glu Pro Arg Cys Lys Phe Gly Glu Cys Val Gly
            85                  90                  95
Pro Asn Lys Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser
            100                 105                 110
Gln Asp Val Asn Glu Cys Ala Phe Lys Pro Arg Pro Cys Gln His Arg
        115                 120                 125
Cys Val Asn Thr His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His
    130                 135                 140
Met Leu Leu Pro Asp Ala Thr Cys Ser Asn Ser Arg Thr Cys Ala Arg
145                 150                 155                 160
```

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1011c2PCTSEQUENCE LISTING

```
Ile Asn Cys Gln Tyr Ser Cys Glu Asp Thr Ala Glu Gly Pro Arg Cys
                165             170             175
Val Cys Pro Ser Ser Gly Leu Arg Leu Gly Pro Asn Gly Arg Val Cys
            180             185             190
Leu Asp Ile Asp Glu Cys Ala Ser Ser Lys Ala Val Cys Pro Ser Asn
            195             200             205
Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys Cys His Ile
    210             215             220
Gly Phe Glu Leu Lys Tyr Ile Ser Arg Arg Tyr Asp Cys Val Asp Ile
225             230             235             240
Asn Glu Cys Thr Leu Asn Thr Arg Thr Cys Ser Pro His Ala Asn Cys
            245             250             255
Leu Asn Thr Gln Gly Ser Phe Lys Cys Lys Cys Lys Gln Gly Tyr Arg
            260             265             270
Gly Asn Gly Leu Gln Cys Ser Val Ile Pro Glu His
            275             280
```

```
<210> 390
<211> 85
<212> PRT
<213> Rat
```

```
<400> 390
Gly Ala Pro Met Tyr Phe Ser Glu Gly Arg Glu Arg Gly Lys Val Tyr
1               5               10              15
Val Tyr Asn Leu Arg Gln Asn Arg Phe Val Phe Asn Gly Thr Leu Lys
            20              25              30
Asp Ser His Ser Tyr Gln Asn Ala Arg Phe Gly Ser Cys Ile Ala Ser
        35              40              45
Val Gln Asp Leu Asn Gln Asp Ser Tyr Asn Asp Val Val Val Gly Ala
    50              55              60
Pro Gln Glu Asp Ser His Arg Gly Ala Ile Tyr Ile Phe His Gly Phe
65              70              75              80
Gln Thr Asn Ile Leu
                85
```

```
<210> 391
<211> 158
<212> PRT
<213> Rat
```

```
<400> 391
Phe Gln Thr Asn Ile Leu Lys Lys Pro Val Gln Arg Ile Ser Ala Ser
1               5               10              15
Glu Leu Ala Pro Gly Leu Gln His Phe Gly Cys Ser Ile His Gly Gln
            20              25              30
Leu Asp Leu Asn Glu Asp Gly Leu Val Asp Leu Ala Val Gly Ala Leu
        35              40              45
Gly Asn Ala Val Val Leu Trp Ala Arg Pro Val Val Gln Ile Asn Ala
    50              55              60
Ser Leu His Phe Glu Pro Ser Lys Ile Asn Ile Phe His Lys Asp Cys
65              70              75              80
Lys Arg Asn Gly Arg Asp Ala Thr Cys Leu Ala Ala Phe Leu Cys Phe
            85              90              95
Gly Pro Ile Phe Leu Ala Pro His Phe His Thr Ala Thr Val Gly Ile
```

1011c2PCTSEQUENCE LISTING

```
                100                        105                     110
Arg Tyr Asn Ala Thr Met Asp Glu Arg Arg Tyr Met Pro Arg Ala His
                115                        120                     125
Leu Asp Glu Gly Ala Asp Gln Phe Thr Asn Arg Ala Val Leu Leu Ser
                130                        135                     140
Ser Gly Gln Glu His Cys Gln Arg Ile Asn Phe His Val Leu
145                        150                        155
```

```
        <210> 392
        <211> 124
        <212> PRT
        <213> Mouse


        <400> 392
Ala Ala Glu Gln Glu Ala Ser Ser Arg Arg Arg Gly Gly Ala Gly
1                   5                   10                  15
Pro Ala Leu Phe Ser Ser Gly Ser Leu Arg Ser Glu Pro Gln Pro Arg
                20                      25                      30
Leu Pro Gln Ala Arg Ser Arg Pro Arg Pro Ser Phe Leu Gln Ala Arg
        35                      40                      45
Ser Arg Pro Cys Leu Ser Gln Ala Cys Ser Pro Ala Ala Ser Val Leu
        50                      55                          60
Ser Ser Ser Ser Leu Cys Gly Arg Ser His Leu Leu Pro Gly Ser Leu
65                      70                      75                  80
Pro Ala Thr Ala Phe Leu Leu Leu Leu Pro Gly Ser Leu Pro Gly Arg
                85                      90                      95
Arg Pro Ser Ala Ala Gln Ala Ala Pro Val Leu Ala Trp Gly Leu Val
                100                     105                     110
Ala Phe Gln Leu Gly Val Ala Ala Gly Ala Gly Arg
        115                     120
```

```
        <210> 393
        <211> 242
        <212> PRT
        <213> Rat


        <400> 393
Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys Gly Gln
1                   5                   10                  15
Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ser Ser His Leu Val
                20                      25                      30
Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Thr Gly Pro Glu Glu
        35                      40                      45
Ser His Cys Leu Gln Cys Arg Lys Gly Trp Ala Leu His His Leu Lys
        50                      55                      60
Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gln Ala Thr Cys Gly Ala
65                      70                      75                  80
Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg Asp Cys
                85                      90                      95
Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Pro Cys Lys
                100                     105                     110
Lys Cys Ser Arg Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu Asp Val
        115                     120                     125
Asp Glu Cys Glu Thr Val Val Cys Pro Gly Glu Asn Glu Gln Cys Glu
        130                     135                     140
```

1011c2PCTSEQUENCE LISTING

```
Asn Thr Glu Gly Ser Tyr Arg Cys Val Cys Ala Glu Gly Phe Arg Gln
145             150             155             160
Glu Asp Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala Gly Phe
                165             170             175
Phe Ala Glu Met Thr Glu Asp Glu Met Val Val Leu Gln Gln Met Phe
            180             185             190
Phe Gly Val Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys Gly Asp
        195             200             205
Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met Thr Gly
    210             215             220
Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe Ile Lys
225             230             235             240
Gly Arg
```

```
<210> 394
<211> 99
<212> PRT
<213> Mouse
```

```
<400> 394
Met Arg Leu Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Cys
1               5               10              15
Ala Ser Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro
            20              25              30
Lys Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr
        35              40              45
Pro His Cys Glu Glu Lys Met Val Ile Val Thr Thr Lys Ser Met Ser
    50              55              60
Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr
65              70              75              80
Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val
            85              90              95
Tyr Glu Glu
```

```
<210> 395
<211> 103
<212> PRT
<213> Human
```

```
<400> 395
Met Ala Leu Gly Val Pro Ile Ser Val Tyr Leu Leu Phe Asn Ala Met
1               5               10              15
Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
            20              25              30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile
        35              40              45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
    50              55              60
Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
65              70              75              80
Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn Val Cys
            85              90              95
Ser Gly Glu Arg Arg Pro Leu
```

1011c2PCTSEQUENCE LISTING
100

<210> 396
<211> 1529
<212> PRT
<213> Rat

<400> 396

```
Met Ser Gly Ile Gly Trp Gln Thr Leu Ser Leu Ser Leu Ala Leu Val
1               5                   10                  15
Leu Ser Ile Leu Asn Lys Val Ala Pro His Ala Cys Pro Ala Gln Cys
            20                  25                  30
Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
        35                  40                  45
Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
    50                  55                  60
Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
65                  70                  75                  80
Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
                85                  90                  95
Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
            100                 105                 110
Asn Asn Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys
        115                 120                 125
Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
    130                 135                 140
Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
145                 150                 155                 160
Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
                165                 170                 175
Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
                180                 185                 190
Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
            195                 200                 205
Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
        210                 215                 220
Arg Gln Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
225                 230                 235                 240
His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
                245                 250                 255
Cys Ser Gly His Gln Ser Phe Met Ala Pro Ser Cys Ser Val Leu His
            260                 265                 270
Cys Pro Ile Ala Cys Thr Cys Ser Asn Asn Ile Val Asp Cys Arg Gly
        275                 280                 285
Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu Thr Ile Thr Glu
    290                 295                 300
Ile Arg Leu Glu Gln Asn Ser Ile Arg Val Ile Pro Pro Gly Ala Phe
305                 310                 315                 320
Ser Pro Tyr Lys Lys Leu Arg Arg Leu Asp Leu Ser Asn Asn Gln Ile
                325                 330                 335
Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg Ser Leu Asn Ser
            340                 345                 350
Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro Lys Ser Leu Phe
            355                 360                 365
Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys Ile
```

1011c2PCTSEQUENCE LISTING

```
        370                     375                      380
Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His Asn Leu Asn Leu
385                     390                      395                  400
Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Val Ala Lys Gly Thr Phe
                    405                 410                  415
Ser Ala Leu Arg Ala Ile Gln Thr Met His Leu Ala Gln Asn Pro Phe
                420                 425                  430
Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr Leu His Thr Asn
                435                 440                  445
Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro Arg Arg Leu Ala
        450                 455                  460
Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe Arg Cys Ser Ala
465                     470                  475                      480
Lys Glu Gln Tyr Phe Ile Pro Gly Thr Glu Asp Tyr Arg Ser Lys Leu
                485                 490                  495
Ser Gly Asp Cys Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys
                500                 505                  510
Glu Gly Thr Thr Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro
                515                 520                  525
Asp His Ile Pro Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu
        530                 535                  540
Phe Thr Val Leu Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu
545                     550                  555                      560
Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly
                565                 570                  575
Ala Phe Glu Gly Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn
                580                 585                  590
Arg Leu Glu Asn Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu
                595                 600                  605
Lys Thr Leu Met Leu Arg Ser Asn Arg Ile Ser Cys Val Gly Asn Asp
        610                 615                  620
Ser Phe Thr Gly Leu Gly Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn
625                     630                  635                      640
Gln Ile Thr Thr Val Ala Pro Gly Ala Phe Gly Thr Leu His Ser Leu
                645                 650                  655
Ser Thr Leu Asn Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys His Leu
                660                 665                  670
Ala Trp Leu Gly Glu Trp Leu Arg Arg Lys Arg Ile Val Thr Gly Asn
                675                 680                  685
Pro Arg Cys Gln Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp
        690                 695                  700
Val Ala Ile Gln Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser
705                     710                  715                      720
Cys Ser Pro Leu Ser Arg Cys Pro Ser Glu Cys Thr Cys Leu Asp Thr
                725                 730                  735
Val Val Arg Cys Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile
                740                 745                  750
Pro Arg Asp Val Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu
                755                 760                  765
Val Pro Lys Glu Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu
        770                 775                  780
Ser Asn Asn Arg Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met
785                     790                  795                      800
Thr Gln Leu Leu Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile
                805                 810                  815
```

1011c2PCTSEQUENCE LISTING

```
Pro Pro Arg Thr Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu
        820             825             830
His Gly Asn Asp Ile Ser Val Val Pro Glu Gly Ala Phe Gly Asp Leu
        835             840             845
Ser Ala Leu Ser His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp
    850             855             860
Cys Asn Met Gln Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu
865             870             875             880
Pro Gly Ile Ala Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu
            885             890             895
Leu Leu Thr Thr Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp
        900             905             910
Val Thr Ile Gln Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys
        915             920             925
Asn Asp Gly Thr Cys Asn Asn Asp Pro Val Asp Phe Tyr Arg Cys Thr
    930             935             940
Cys Pro Tyr Gly Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala
945             950             955             960
Cys Ile Ser Asn Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu
            965             970             975
Gly Glu Asn Asp Gly Phe Trp Cys Thr Cys Ala Asp Gly Phe Glu Gly
            980             985             990
Glu Ser Cys Asp Ile Asn Ile Asp Asp Cys Glu Asp Asn Asp Cys Glu
        995             1000            1005
Asn Asn Ser Thr Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys
    1010            1015            1020
Pro Pro Glu Tyr Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys
1025            1030            1035            104
Ala Gln Asp Leu Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr
            1045            1050            1055
Pro Lys Gly Phe Lys Cys Asp Cys Thr Pro Gly Tyr Ile Gly Glu His
            1060            1065            1070
Cys Asp Ile Asp Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly
        1075            1080            1085
Ala His Cys Thr Asp Ala Val Asn Gly Tyr Thr Cys Val Cys Pro Glu
    1090            1095            1100
Gly Tyr Ser Gly Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Leu
1105            1110            1115            112
Arg Thr Ser Pro Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys
            1125            1130            1135
Ile Ile Arg Val Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Leu
        1140            1145            1150
Gly Glu Lys Cys Glu Lys Leu Val Ser Val Asn Phe Val Asn Lys Glu
        1155            1160            1165
Ser Tyr Leu Gln Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile
    1170            1175            1180
Thr Leu Gln Ile Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys
1185            1190            1195            120
Gly Asp Lys Asp His Ile Ala Val Glu Leu Tyr Arg Gly Arg Val Arg
            1205            1210            1215
Ala Ser Tyr Asp Thr Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val
    1220            1225            1230
Glu Thr Ile Asn Asp Gly Asn Phe His Ile Val Glu Leu Leu Thr Leu
    1235            1240            1245
Asp Ser Ser Leu Ser Leu Ser Val Asp Gly Gly Ser Pro Lys Ile Ile
```

1011c2PCTSEQUENCE LISTING

```
      1250                    1255                    1260
Thr Asn Leu Ser Lys Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr
1265                    1270                    1275                    128
Val Gly Gly Met Pro Gly Lys Asn Asn Val Ala Ser Leu Arg Gln Ala
                  1285                    1290                    1295
Pro Gly Gln Asn Gly Thr Ser Phe His Gly Cys Ile Arg Asn Leu Tyr
                  1300                    1305                    1310
Ile Asn Ser Glu Leu Gln Asp Phe Arg Lys Val Pro Met Gln Thr Gly
                  1315                    1320                    1325
Ile Leu Pro Gly Cys Glu Pro Cys His Lys Lys Val Cys Ala His Gly
                  1330                    1335                    1340
Thr Cys Gln Pro Ser Ser Gln Ser Gly Phe Thr Cys Glu Cys Glu Glu
1345                    1350                    1355                    136
Gly Trp Met Gly Pro Leu Cys Asp Gln Arg Thr Asn Asp Pro Cys Leu
                  1365                    1370                    1375
Gly Asn Lys Cys Val His Gly Thr Cys Leu Pro Ile Asn Ala Phe Ser
                  1380                    1385                    1390
Tyr Ser Cys Lys Cys Leu Glu Gly His Gly Gly Val Leu Cys Asp Glu
                  1395                    1400                    1405
Glu Glu Asp Leu Phe Asn Pro Cys Gln Val Ile Lys Cys Lys His Gly
                  1410                    1415                    1420
Lys Cys Arg Leu Ser Gly Leu Gly Gln Pro Tyr Cys Glu Cys Ser Ser
1425                    1430                    1435                    144
Gly Phe Thr Gly Asp Ser Cys Asp Arg Glu Ile Ser Cys Arg Gly Glu
                  1445                    1450                    1455
Arg Ile Arg Asp Tyr Tyr Gln Lys Gln Gln Gly Tyr Ala Ala Cys Gln
                  1460                    1465                    1470
Thr Thr Lys Lys Val Ser Arg Leu Glu Cys Arg Gly Gly Cys Ala Gly
                  1475                    1480                    1485
Gly Gln Cys Cys Gly Pro Leu Arg Ser Lys Arg Arg Lys Tyr Ser Phe
                  1490                    1495                    1500
Glu Cys Thr Asp Gly Ser Ser Phe Val Asp Glu Val Glu Lys Val Val
1505                    1510                    1515                    152
Lys Cys Gly Cys Thr Arg Cys Ala Ser
                  1525
```

        <210> 397
        <211> 8
        <212> PRT
        <213> Mouse

        <400> 397
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Trp Tyr Asn Ala Trp Asn Glu Lys
 1               5
```

        <210> 398
        <211> 7
        <212> PRT
        <213> Mouse

        <400> 398
```
Met Val Ile Ile Thr Thr Lys
 1               5
```

        <210> 399

1011c2PCTSEQUENCE LISTING

&lt;211&gt; 2206
&lt;212&gt; DNA
&lt;213&gt; Rat

&lt;400&gt; 399

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60
tggaacatct cagcccacac agactaagcg gagactgatg ttggtggcgt tcctcggagc
120
atccgcggtg actgcaagta ccggtctcct gtggaagaag gctcacgcag aatctccacc
180
gagcgtcaac agcaagaaga ctgacgctgg agataagggg aagagcaagg acacccggga
240
agtgtccagc catgaaggaa gcgctgcaga cactgcggcc gagccttacc cagaggagaa
300
gaagaagaag cgttctggat tcagagacag aaaagtaatg gagtatgaga ataggatccg
360
agcctactcc acaccagaca aaatcttccg gtattttgcc accttgaaag taatcaacga
420
acctggtgaa actgaagtgt tcatgacccc acaggacttt gtgcgctcca taacacccaa
480
tgagaagcag ccagaacact tgggcctgga tcagtacata ataaagcgct tcgatggaaa
540
gaaaattgcc caggaacgag aaaagtttgc tgacgaaggc agcatcttct ataccttgg
600
agagtgtgga ctcatctcct tctctgacta catcttcctc acaacggtgc tctccactcc
660
tcagagaaat ttcgaaattg ccttcaagat gtttgacttg aatggagatg gagaagtaga
720
catggaggag tttgagcagg ttcaaagcat cattcgctcc cagaccagca tgggcatgcg
780
tcacagagat cgtccaacta ctgggaacac cctcaagtct ggcttatgtt cggccctcac
840
gacctacttt tttggagctg atctcaaagg gaaactgacc attaaaaact tcctggaatt
900
tcagcgtaaa ctgcagcatg acgttctaaa gctggagttt gaacgccatg acccggtaga
960
cgggagaatc tctgagaggc agttcggtgg catgctgctg gcctacagtg gagtgcagtc
1020
caagaagctg accgccatgc agaggcagct gaagaagcac ttcaaggatg ggaagggcct
1080
gactttccag gaggtggaga acttcttcac tttcctgaag aacattaatg acgtggacac
1140
tgcgttaagc ttttaccaca tggctggagc atccctcgat aaagtgacca tgcagcaagt
1200
ggccaggaca gtggcgaaag tcgagctgtc ggaccacgtg tgtgacgtgg tgtttgcact
1260
ctttgactgc gacggcaatg gggagctgag caataaggag tttgtctcca tcatgaagca
1320
gcggctgatg agaggcctgg agaagcccaa ggacatgggc tttacccgtc tcatgcaggc
1380
catgtggaaa tgtgcccaag aaaccgcctg gactttgct ctacccaaat agtaccccac
1440
ctcctgcacc ttagcacccc gcaatcctgg agtggccttc atgctgctga tgcttctggg
1500
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1011c2PCTSEQUENCE LISTING
agtagtgccc acatccccat ctttctggaa gtgacctctg gcctcagctg gctgacctct
    1560
ccatcctccc ctgacccagt cagtgttccg ctaggctctg aatctgcagt cagatcaaag
    1620
gtctaagaca ggaacaagtc ttcaaagcag agaccatagc tcccttaacc agtgccccgt
    1680
gggtaaatgc ggggagccct cccacactgg cagccccagg aggcatctct gcagtctctc
    1740
actgtggatt taagtaacac aaacgtccct gccatcttcc tcccactgtt ttaaagctgc
    1800
aagtttggaa atactctggc aggcaaaggg aagtctgtga tgaacggtaa tgcagatgac
    ·1860
cctggtaccc tgatctggca gggcacctgg tcaggggaag ggtctgcgtc agacaccagc
    1920
ggcaccagga aggctctttg ccaccagcac agctcccgat tcaaagtcgc tgctttgagc
    1980
ggctctccag aacctcctgc tctttttttt ttcctcccgg ctccctgcga tgcctcctct
    2040
gggactctgc ttcactagag ccagggctga gccctgttc cttgtgtctt gtccctctc
    2100
tatagacctg cagagcgcag ctcagagcct atctgccctc tgtctaatac actcgtaaat
    2160
atcactttaa ttatagcact ttgcaggaaa taccccaaaa aaaaaa
    2206

        <210> 400
        <211> 160
        <212> DNA
        <213> Mouse

        <400> 400
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        60
tctctttctc ttttttctgtt tcttgttccc ctttccccctt ·ttcctggtga gaaagcacat
        120
attactgagc cattgcaagc aatgggaggg gtccacaatg
        160

        <210> 401
        <211> 430
        <212> DNA
        <213> Rat

        <400> 401
ggcaccagcc cggcttctgt gctccgctca gtctccagcg atccctccct acctccgccc
        60
tccatggcgt cgctcctgtg ctgtgggcct aagctggccg cctgtggcat cgtcctcagc
        120
gcctggggag tgatcatgtt gataatgctc gggatatttt tcaatgtcca ttctgctgtg
        180
ttaattgagg atgtccccctt cacagagaaa gattttgaga acggccctca gaacatatac
        240
aacctgtacg agcaagtcag ctacaactgt ttcatcgccg cgggcctcta cctcctcctc
        300
gggggcttct ccttctgcca agttcgtctc aataagcgca aggaatacat ggtgcgctag

1011c2PCTSEQUENCE LISTING

         360
agcgcagtcc gactctcccc attcccctcc ttatttaaag actcctcagt ccatctgttc
         420
cactcatctg
         430


         <210> 402
         <211> 190
         <212> DNA
         <213> Rat

         <400> 402
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         60
ttgcacactg aattgaagaa atgttggttt ttcttgtttt gttttagttt gtttctttgg
         120
ttttgttttt ggttttgctt tttacttccc aggtttgact atttgccaat gccgtcgacg
         180
cggccgcgaa
         190


         <210> 403
         <211> 1774
         <212> DNA
         <213> Mouse

         <400> 403
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         60
ccggcgaatt cgcaggctgg gagaaggtgg gctcgggcgg cttcgggcag gtgtacaagg
         120
tgcgccatgt gcactggaag acgtggctcg cgatcaagtg ctcgcccagt ctgcacgtcg
         180
acgacaggga acgaatggag ctcctggagg aagctaagaa gatggagatg gccaagttcc
         240
gatacattct acctgtgtac ggcatatgcc aggaacctgt cggcttggtc atggagtaca
         300
tggagacagg ctccctggag aagctgctgg cctcagagcc attgccttgg gacctgcgct
         360
ttcgcatcgt gcacgagaca gccgtgggca tgaacttcct gcattgcatg tctccgccac
         420
tgctgcacct agacctgaag ccagcgaaca tcctgctgga tgcccactac catgtcaaga
         480
tttctgactt tgggctggcc aagtgcaatg gcatgtccca ctctcatgac ctcagcatgg
         540
atggcctgtt tggtacaatc gcttacctcc ctccagagcg aattcgtgag aagagccgct
         600
tgtttgacac caaacatgat gtatacagct cgccattgt gatctggggt gtgcttacac
         660
agaagaagcc atttgcagat gaaaagaaca tcctacacat catgatgaaa gtggtaaagg
         720
gccaccgccc agagctgcca cccatctgca gaccccggcc gcgtgcctgt gccagcctga
         780
tagggataat gcaacggtgc tggcatgcag acccacaggt gcggcccacc ttccaagaaa
         840

1011c2PCTSEQUENCE LISTING
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ttacctctga aacagaagac ctttgtgaga agcctgatga ggaggtgaaa gacctggctc
   900
atgagccagg cgagaaaagc tctctagagt ccaagagtga ggccaggccc gagtcctcac
   960
gcctcaagcg cgcctctgct ccccccttcg ataacgactg cagtctctcc gagttgctgt
  1020
cacagttgga ctctgggatc tcccagactc ttgaaggccc cgaagagctc agccgaagtt
  1080
cctctgaatg caagctccca tcgtccagca gtggcaagag gctctcgggg gtgtcctcag
  1140
tggactcagc ctttttcctcc agaggatcgc tgtcactgtc ttttgagcgg gaagcttcaa
  1200
caggcgacct gggccccaca gacatccaga agaagaagct agtggatgcc atcatatcag
  1260
gggacaccag caggctgatg aagatcctac agccccaaga tgtggacttg gttctagaca
  1320
gcagtgccag cctgctgcac ctggctgtgg aggccggaca ggaggagtgt gtcaagtggc
  1380
tgctgcttaa caatgccaac cccaacctga ccaacaggaa gggctctaca ccactgcata
  1440
tggctgtgga gcggaaggga cgtggaattg tggagctact gctagcccgg aagaccagtg
  1500
tcaatgccaa ggatgaagac cagtggactg ccctgcactt tgcagcccag aatggggatg
  1560
aggccagcac aaggctgctg ctagagaaga atgcttctgt caatgaggtg gactttgagg
  1620
gccgaacacc catgcatgta gcctgccagc atggacagga gaacattgtg cgcaccctgc
  1680
tccgccgtgg tgtggatgtg ggcctgcagg gaaaggatgc ctggttgcct ctgcactatg
  1740
ctgcctggca aggccacctt cccattggta agct
  1774
```

        <210> 404
        <211> 372
        <212> DNA
        <213> Mouse


        <400> 404
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ccacagcaca tcgtcctgac tgtcctcttc ccagggacca agagctagag acccggctgt
   60
gactgcccgc ctctggggct tcctttagag gagacagtct ttacccatct agactcctgc
  120
caccctgact gctgacttac agctatgagg tcccggcttc tgctgcccgt gccccatttg
  180
ccaacgattc gggaaatgtc agaagagctg tcacatgggg cagctgggca ggaacccca
  240
gcgtccccca gcctggatga ctacgtcagg tgtatctgtc agctggcaca gcccacctca
  300
gtgctggaca aggtcacagc ccagagccgt cccaacagac cctcccggcc agcctggact
  360
cgagagaaga gg
  372
```

        <210> 405

1011c2PCTSEQUENCE LISTING
<211> 396
<212> DNA
<213> Mouse

<400> 405
gagcttcgaa gctttctccg tcttccaaga cgacaggttt ctggggccac aagaggccga
      60
gcctcttcat tttgttttct tctccaggct gaagacctga acgtcaagtt ggaaggggag
      120
ccttccatgc ggaaaccaaa gcagcggccg cggccggagc ccctcatcat ccccaccaag
      180
gcgggcactt tcatcgcccc tcctgtctac tccaacatca ccccttacca gagccacctg
      240
cgctctcccg tgcgccttgc tgaccacccc tctgagcgga gctttgagcc ccccccttac
      300
acaccacccc ccattctcag ccccgtccgg gaaggctctg gcctctactt caatgccatc
      360
atatcaacca gcaacatccc ggcccctcct gtatca
      396


<210> 406
<211> 444
<212> PRT
<213> Rat


<400> 406
Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr Gly
 1               5                   10                  15
Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Ser Val Asn Ser
            20                  25                  30
Lys Lys Thr Asp Ala Gly Asp Lys Gly Lys Ser Lys Asp Thr Arg Glu
        35                  40                  45
Val Ser Ser His Glu Gly Ser Ala Ala Asp Thr Ala Ala Glu Pro Tyr
    50                  55                  60
Pro Glu Glu Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val
65                  70                  75                  80
Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile
                85                  90                  95
Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu Thr
            100                 105                 110
Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro Asn
            115                 120                 125
Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg
        130                 135                 140
Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp Glu
145                 150                 155                 160
Gly Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser
                165                 170                 175
Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe
            180                 185                 190
Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp
            195                 200                 205
Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser
        210                 215                 220
Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys

1011c2PCTSEQUENCE LISTING
```
225                    230                 235                    240
Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu
                245                 250                    255
Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu
                260                 265                    270
Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp
            275                 280                    285
Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser
        290                 295                    300
Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys
305                 310                 315                    320
His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe
                325                 330                    335
Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe
            340                 345                    350
Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val
        355                 360                    365
Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val
    370                 375                    380
Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys
385                 390                 395                    400
Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys
                405                 410                    415
Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys
            420                 425                    430
Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys
        435                 440
```

```
        <210> 407
        <211> 53
        <212> PRT
        <213> Mouse


        <400> 407
Arg Arg Thr Leu Thr Gly Gln Leu Gly Leu Phe Ser Val Asp Phe Met
1                 5                 10                   15
Val Cys Ile Phe Leu Phe Leu Phe Phe Cys Phe Leu Phe Pro Phe Pro
                20                 25                   30
Leu Phe Leu Val Arg Lys His Ile Leu Leu Ser His Cys Lys Gln Trp
            35                 40                   45
Glu Gly Ser Thr Met
        50


        <210> 408
        <211> 119
        <212> PRT
        <213> Rat


        <400> 408
Gly Thr Ser Pro Ala Ser Val Leu Arg Ser Val Ser Ser Asp Pro Ser
1                 5                 10                   15
Leu Pro Pro Pro Ser Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu
            20                 25                   30
Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile
        35                 40                   45
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1011c2PCTSEQUENCE LISTING

```
Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp
    50              55              60
Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr
65              70              75              80
Asn Leu Tyr Glu Gln Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu
            85              90                  95
Tyr Leu Leu Leu Gly Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys
        100             105                 110
Arg Lys Glu Tyr Met Val Arg
        115
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<210> 409
<211> 590
<212> PRT
<213> Mouse


<400> 409
Lys Val Glu Gly Glu Gly Arg Gly Arg Trp Ala Leu Gly Leu Leu Arg
1               5               10              15
Thr Phe Asp Ala Gly Glu Phe Ala Gly Trp Glu Lys Val Gly Ser Gly
            20              25              30
Gly Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp
        35              40              45
Leu Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg
    50              55              60
Met Glu Leu Leu Glu Glu Ala Lys Lys Met Glu Met Ala Lys Phe Arg
65              70              75              80
Tyr Ile Leu Pro Val Tyr Gly Ile Cys Gln Glu Pro Val Gly Leu Val
            85              90                  95
Met Glu Tyr Met Glu Thr Gly Ser Leu Glu Lys Leu Leu Ala Ser Glu
        100             105                 110
Pro Leu Pro Trp Asp Leu Arg Phe Arg Ile Val His Glu Thr Ala Val
        115             120                 125
Gly Met Asn Phe Leu His Cys Met Ser Pro Pro Leu Leu His Leu Asp
    130             135                 140
Leu Lys Pro Ala Asn Ile Leu Leu Asp Ala His Tyr His Val Lys Ile
145             150             155                 160
Ser Asp Phe Gly Leu Ala Lys Cys Asn Gly Met Ser His Ser His Asp
            165             170                 175
Leu Ser Met Asp Gly Leu Phe Gly Thr Ile Ala Tyr Leu Pro Pro Glu
        180             185                 190
Arg Ile Arg Glu Lys Ser Arg Leu Phe Asp Thr Lys His Asp Val Tyr
    195             200                 205
Ser Phe Ala Ile Val Ile Trp Gly Val Leu Thr Gln Lys Lys Pro Phe
    210             215                 220
Ala Asp Glu Lys Asn Ile Leu His Ile Met Met Lys Val Val Lys Gly
225             230             235                 240
His Arg Pro Glu Leu Pro Pro Ile Cys Arg Pro Arg Pro Arg Ala Cys
            245             250                 255
Ala Ser Leu Ile Gly Ile Met Gln Arg Cys Trp His Ala Asp Pro Gln
        260             265                 270
Val Arg Pro Thr Phe Gln Glu Ile Thr Ser Glu Thr Glu Asp Leu Cys
    275             280                 285
Glu Lys Pro Asp Glu Glu Val Lys Asp Leu Ala His Glu Pro Gly Glu
    290             295                 300
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1011c2PCTSEQUENCE LISTING

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Lys Ser Ser Leu Glu Ser Lys Ser Glu Ala Arg Pro Glu Ser Ser Arg
305                 310             315             320
Leu Lys Arg Ala Ser Ala Pro Pro Phe Asp Asn Asp Cys Ser Leu Ser
                325             330             335
Glu Leu Leu Ser Gln Leu Asp Ser Gly Ile Ser Gln Thr Leu Glu Gly
            340             345             350
Pro Glu Glu Leu Ser Arg Ser Ser Glu Cys Lys Leu Pro Ser Ser
        355             360             365
Ser Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val Asp Ser Ala Phe
    370             375             380
Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg Glu Ala Ser Thr
385             390             395             400
Gly Asp Leu Gly Pro Thr Asp Ile Gln Lys Lys Lys Leu Val Asp Ala
                405             410             415
Ile Ile Ser Gly Asp Thr Ser Arg Leu Met Lys Ile Leu Gln Pro Gln
            420             425             430
Asp Val Asp Leu Val Leu Asp Ser Ser Ala Ser Leu Leu His Leu Ala
        435             440             445
Val Glu Ala Gly Gln Glu Glu Cys Val Lys Trp Leu Leu Leu Asn Asn
    450             455             460
Ala Asn Pro Asn Leu Thr Asn Arg Lys Gly Ser Thr Pro Leu His Met
465             470             475             480
Ala Val Glu Arg Lys Gly Arg Gly Ile Val Glu Leu Leu Leu Ala Arg
                485             490             495
Lys Thr Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr Ala Leu His
            500             505             510
Phe Ala Ala Gln Asn Gly Asp Glu Ala Ser Thr Arg Leu Leu Leu Glu
        515             520             525
Lys Asn Ala Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met
    530             535             540
His Val Ala Cys Gln His Gly Gln Glu Asn Ile Val Arg Thr Leu Leu
545             550             555             560
Arg Arg Gly Val Asp Val Gly Leu Gln Gly Lys Asp Ala Trp Leu Pro
                565             570             575
Leu His Tyr Ala Ala Trp Gln Gly His Leu Pro Ile Gly Lys
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    120
aacaaaacag aagctgacaa catagaagga cccatagcct tgaagttctc acacctttgc
    180
ctggaagatc ataacagtta ctgcatcaac ggtgcttgtg cattccacca tgagctagag
    240
aaagccatct gcaggtgttt tactggttat actggagaaa ggtgtctaaa attgaaatcg
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1011c2PCTSEQUENCE LISTING

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    120
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    180
aacggtgctt gtgcattcca ccatgagcta gagaaagcca tctgcaggtg tctaaaattg
    240
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        <212> DNA
        <213> Human

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    120
ctggaagatc ataacagtta ctgcatcaac ggtgcttgtg cattccacca tgagctagag
    180
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    240
cgaccactgt gaggcctttg tgaagaattt tcatcaaggc atctgtagag atcagtgagc
    300
ccaaaattaa agttttcaga tgaaacaaca aaacttgtca agctgactag actcgaaaat
    360
aatgaaagtt gggatcacaa tgaaatgaga agataaaatt cagcgttggc ctttagactt
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        <210> 413
        <211> 112
        <212> PRT
        <213> Human

        <400> 413
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            20                25                30
Ala Gln Gln Gly Asn Trp Thr Val Asn Lys Thr Glu Ala Asp Asn Ile
        35                40                45
Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu Asp His
    50                55                60

1011c2PCTSEQUENCE LISTING

Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu Leu Glu
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Lys Leu Lys Ser Pro Tyr Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
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            20                  25                  30
Ala Gln Gln Ala Asp Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser
            35                  40                  45
His Leu Cys Leu Glu Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys
    50                  55                  60
Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg Cys Leu Lys Leu
65                  70                  75                  80
Lys Ser Pro Tyr Asn Val Cys Ser Gly Glu Arg Arg Pro Leu
                85                  90

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Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser His Leu Cys Leu Glu
            20                  25                  30
Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys Ala Phe His His Glu
            35                  40                  45
Leu Glu Lys Ala Ile Cys Arg Cys Leu Lys Leu Lys Ser Pro Tyr Asn
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Val Cys Ser Gly Glu Arg Arg Pro Leu
65                  70

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        <212> DNA
        <213> Human

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    120
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    180

1011c2PCTSEQUENCE LISTING
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cgaccactgt ga
    312


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        <211> 103
        <212> PRT
        <213> Human


        <400> 417
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Thr Ala Leu Thr Glu Glu Ala Ala Val Thr Val Thr Pro Pro Ile Thr
             20                  25                  30
Ala Gln Gln Ala Asp Asn Ile Glu Gly Pro Ile Ala Leu Lys Phe Ser
         35                  40                  45
His Leu Cys Leu Gly Asp His Asn Ser Tyr Cys Ile Asn Gly Ala Cys
     50                  55                  60
Ala Phe His His Glu Leu Glu Lys Ala Ile Cys Arg Cys Phe Thr Gly
65                  70                  75                  80
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        <212> DNA
        <213> Rat


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    120
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    480
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1011c2PCTSEQUENCE LISTING
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        <210> 419
        <211> 960
        <212> DNA
        <213> Mouse


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        <212> DNA
        <213> Mouse


        <400> 420

1011c2PCTSEQUENCE LISTING

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    720
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   1080
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   1260
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   1320
aaaaaaaaaa
   1330
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     <212> DNA
     <213> Mouse

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     60
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1011c2PCTSEQUENCE LISTING

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    180
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    300
ctctcacatt gtcagtgtac agcttggtgg cctttgtcac tggcatgctc tgtgacactg
    360
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    420
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        <213> Mouse

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    420
aaggcactgt ttgaagcaca ggccatgaag taagacttgc tttctagtta aattgaggtt
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        <210> 423
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1011c2PCTSEQUENCE LISTING

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<213> Rat

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738

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<211> 1035
<212> DNA
<213> Rat

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1011c2PCTSEQUENCE LISTING

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        <212> DNA
        <213> Rat

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1011c2PCTSEQUENCE LISTING
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       <213> Mouse

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  720
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 1200
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aaaaaaaaaa aaaaaaa
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1011c2PCTSEQUENCE LISTING
1337

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         120
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gccgatatca ttaccttggg ggtcgctttg taccacctgc tctagagaag aagtaccagc
         660
tgaacctgcc atcttaccct gacacagagt gtgtctaccg tctacagtaa gggaggtggg
         720
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         780

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atcattacca atagatatag ttcttcagac acttctggcc tttgcagtta cctgttatgg
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catagttcat atcgcagggg agttcaaaga catggatgcc acttcagaat taaagaataa
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gacatttgat accttaagga atcacccatc tttttatgtg tttaaccatc gtggtcgagt
         300
gctgttccgg ccttcagatg caacaaattc ttcaaaccta gatgcattgt cctctaatac
         360
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         420
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1011c2PCTSEQUENCE LISTING
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460

      &lt;210&gt; 429
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      &lt;212&gt; DNA
      &lt;213&gt; Mouse

      &lt;400&gt; 429
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ctggcattat gaatgcagtg gggtcagtgt gtggtggatg tgtgtactgg gttggctttc
120
ctttttagtt tttttacttt ttagtttagt ttgttctttt ccttccccaa taaatcattc
180
tcacatgctt ccatgtttgt ttctgagagg tgggggctca aatgtataga aagtaggccc
240
cagtccataa ggaggtgtga acacacccc ttactgctta tcacccattt gacaggaacg
300
cccaggaggg gaggggggagg ggaagaggtg agttctgcac agtcggacat ttctgttgct
360
tttgcatgtt taatatagac gttcctgtcg atccttggga gatcatggcc ttcagatatg
420
cacacgacct ttgaattgtg cctactaatt atagcagggg acttgggtac cc
472

      &lt;210&gt; 430
      &lt;211&gt; 954
      &lt;212&gt; DNA
      &lt;213&gt; Mouse

      &lt;400&gt; 430
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tctctctcat tcccctgctc tgcatcctga tgagaaactg tttggctttt aaaaatgatg
120
ccacagaaat cctttattca catgtggtta aacctgtccc ggcacacccc agcagcaaca
180
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240
acagtcgagt tcaagtgggc tgcagggaac tgcggtccac caaatacatt tcggacggcc
300
agtgcaccag catcagccct ctgaaggagc tggtgtgcgc gggcgagtgc ttgcccctgc
360
cggtgcttcc caactggatc ggaggaggct acggaacaaa gtactggagc cggaggagct
420
ctcaggagtg gcggtgtgtc aacgacaaga cgcgcaccca gaggatccag ctgcagtgtc
480
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600
cccagcacca cagagagcgg aagagagcca gcaaatccag caagcacagt ctgagctaga
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1011c2PCTSEQUENCE LISTING
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        780
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        840
gtttgcagtg aaagccaggc atcctgtagt ttccatcccc tcccccatcc cagtcatttc
        900
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        180
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        420
aaaagaccta acaagcccct cttcactggg ctagtgactc agtgtcagaa aatggacatt
        480
cctttccttg gtgaaatgcc cccagaggat gggatgtaga gaagggaaac cctagcggaa
        540
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        600
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        660
tgaacctgcc atcttaccct gacacagagt gtgtctaccg tctacagtaa gggaggtggg
        720
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        780


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        <212>  DNA
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        120
tatagggagg ttagcacttt ttctaattgg aattcttctc tgtcctgtgg ccccatccct
        180
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1011c2PCTSEQUENCE LISTING
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tcatgcctgt gagtgtgtgg cttgctgtcg tgtcctctgg gatcccaagc cacgcgggtc
    360
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    420
gtggacccag ggtgggttga ttgtctcttt gtaaggaagt atgtgtcggg ggtgacacga
    480
ggctaagccc gagaaacccc gggagacagc actgcataag aaactggttt ccmagactgc
    540
agagggagct gcactttgt tttgaccaaa aacaaaaaac aaaacaaac aaaaacaaaa
    600
caaaaataac tctgaagggc gggaggatac ccaagcctga tgcctgagag gagtccctag
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agcc
    1144
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    120
agctggagtt agagacaatg gtgagctgcc ttgtggatgt tgggaattga acccaggtcc
    180
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    300
gattatttat gaattcaggt ggcttaatgg tatatgcatg aattagtagt aaaacaagaa
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ctagggccag caagtggctt aagggtgcct gctaaccatc tcagccacct gagttcagtc
    420
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1011c2PCTSEQUENCE LISTING

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    120
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    240
gctcctggga gctcaggcga tgagccccca tcgtcctcct cccaagacga ggagttgctg
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        <221> unsure
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        <221> unsure
        <222> (387)...(388)

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    120
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    180
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    240
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    300
ctagcgctaa atggtgtctt taccaacatc ataagactga tagtgngcaa ggncacgccc
    360

aaattgcttc taccgagtgt tccccgnncg ggattgccca ttctt
   405

       <210> 436
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       <212> DNA
       <213> Rat

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       <210> 437
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   900
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1011c2PCTSEQUENCE LISTING

1020

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1140

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1320

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1620

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300

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420

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1011c2PCTSEQUENCE LISTING
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1627

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1011c2PCTSEQUENCE LISTING

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2040
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1011c2PCTSEQUENCE LISTING

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   900
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   1020
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1011c2PCTSEQUENCE LISTING
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      240
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1011c2PCTSEQUENCE LISTING

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    1320
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    1380
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    1440
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    1560
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    1620
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    1680
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    1740
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    1800
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1011c2PCTSEQUENCE LISTING

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1011c2PCTSEQUENCE LISTING
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1011c2PCTSEQUENCE LISTING
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   2100
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        <211> 2250
        <212> DNA
        <213> Mouse

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        <221> unsure
        <222> (2219)...(2219)

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1011c2PCTSEQUENCE LISTING

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1200

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1260

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1320

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1380

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1440

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1860

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1920

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1980

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2040

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2100

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2160

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2220

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          <222> (1482)...(1482)

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1011c2PCTSEQUENCE LISTING
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1011c2PCTSEQUENCE LISTING
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<212> DNA
<213> Rat

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900
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1011c2PCTSEQUENCE LISTING

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     1680
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     1740
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     1800
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     420
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     600
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     720
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1011c2PCTSEQUENCE LISTING
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   1140
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   1200
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   120
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   480
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   600
aagaaagcag aaaacacacg atgggactac ttaactcagg tggaaaaaga atgcaaagag
   660
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   720
aagaaaattt atgaagatgg agatgatgac atgaagcgaa ccattaataa agcgtgggtg
   780
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1011c2PCTSEQUENCE LISTING
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cctcatcgcc agtgatgatg gccgggtttc caggcagccg tggtcctgtc tgaatattgt
   360
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   420
agatagaccc ttg
   433


      &lt;210&gt; 451
      &lt;211&gt; 1225
      &lt;212&gt; DNA
      &lt;213&gt; Mouse


      &lt;400&gt; 451
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   60
cagcagaaac cttcacagac atcttcattt cctggtccgg cccaaggatt ggcaggccat
   120
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   720
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1011c2PCTSEQUENCE LISTING
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   1140
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   1225


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        <212> DNA
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   445


        <210> 453
        <211> 2792
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   300
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1011c2PCTSEQUENCE LISTING

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    1080
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    1140
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    1860
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    1920
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    1980
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1011c2PCTSEQUENCE LISTING

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    2220
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        120
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        600
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1011c2PCTSEQUENCE LISTING
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                1808

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          <212> DNA
          <213> Rat

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                120
agcatgaagc tgctgtgttt ggtggctgtg gtggggtgct tgctggtacc cccggctcaa

1011c2PCTSEQUENCE LISTING

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      240
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      300
gagcccatgc cggtgcctgg ccatgatgtg gaagcctact gcctgctctg tgagtgtagg
      360
tatgaggagc gcagcaccac aaccatcaag gtcattatcg tcatctacct gtctgtggta
      420
ggggcccctct tactctacat ggccttcctg atgctggtgg accctctcat ccgaaagccg
      480
gatgcctata ctgagcagct gcacaatgaa gaagagaatg aggatgcccg ctccatggct
      540
gccgccgccg catccattgg aggaccccga gcaaacaccg tcctggagcg ggtggaaggc
      600
gctcagcagc gatggaagct acaggtgcag gagcagcgga gacggtcttt cgatcgacac
      660
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      720
ttctggggca gtcttccctg ggtcttccct tcaaatgccc gtggcatttg tccttctccc
      780
tctctctaga aatgtactcg actgttataa ctagggagtg ggattgggtc tttggtctct
      840
agtgtctctg taggtctctg gggtagaagg gagggaaagg aaggcagaag agaacagaga
      900
tggttgagac ggccacacga ttggtgaaat tcctccctcc tgtcctcgcc gttcctcaca
      960
gctccacatc ttaaggatgt ttatagctct ttgggagacg gagctgtgcc gtcaatagct
      1020
cggtgggtgc gacgaaagtg tgacccagcc ctcagcctgt gctctacgat gccgtggccc
      1080
ccattcccac ttttncagtg ccaatacttt agcttggcct g
      1121

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            <400> 456
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Leu Arg Leu Ala Trp His Tyr Glu Cys Ser Gly Val Ser Val Trp Trp
            20                  25                  30
Met Cys Val Leu Gly Trp Leu Ser Phe Leu Val Phe Leu Leu Phe Ser
            35                  40                  45
Leu Val Cys Ser Phe Pro Ser Pro Ile Asn His Ser His Met Leu Pro
        50                  55                  60
Cys Leu Phe Leu Arg Gly Gly Gly Ser Asn Val
65                  70                  75

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            <212> PRT
            <213> Rat

1011c2PCTSEQUENCE LISTING

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            20              25              30
Phe Cys Phe Trp Phe Cys Phe Leu Leu Pro Arg Phe Asp Tyr Leu Pro
        35              40              45
Met
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1               5               10              15
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            20              25              30
Cys Gly Gln Gly Ala Ala Cys Asp Pro Val Ser Gly Thr Cys Ile Cys
        35              40              45
Pro Pro Gly Lys Thr Gly Gly His Cys Glu Arg Gly Cys Pro Gln Asp
    50              55              60
Arg Phe Gly Lys Gly Cys Glu His Lys Cys Ala Cys Arg Asn Gly Gly
65              70              75              80
Leu Cys His Ala Thr Asn Gly Ser Cys Ser Cys Pro Leu Gly Trp Met
            85              90              95
Gly Pro His Cys Glu His Ala Cys Pro Ala Gly Arg Tyr Gly Ala Ala
        100             105             110
Cys Leu Leu Glu Cys Ser Cys Gln Asn Asn Gly Ser Cys Glu Pro Thr
    115             120             125
Ser Gly Ala Cys Leu Cys Gly Pro Gly Phe Tyr Gly Gln Ala Cys Glu
    130             135             140
Asp Thr Cys Pro Ala Gly Phe His Gly Ser Gly Cys Gln Arg Val Cys
145             150             155             160
Glu Cys Gln Gln Gly Ala Pro Cys Asp Pro Val Ser Gly Arg Cys Leu
            165             170             175
Cys Pro Ala Gly Phe Arg Gly Gln Phe Cys Glu Arg Gly Cys Lys Pro
        180             185             190
Gly Phe Phe Gly Asp Gly Cys Leu Gln Gln Cys Asn Cys Pro Thr Gly
    195             200             205
Val Pro Cys Asp Pro Ile Ser Gly Leu Cys Leu Cys Pro Pro Gly Arg
    210             215             220
Ala Gly Thr Thr Cys Asp Leu Asp Cys Arg Arg Gly Arg Phe Gly Pro
225             230             235             240
Gly Cys Ala Leu Arg Cys Asp Cys Gly Gly Gly Ala Asp Cys Asp Pro
            245             250             255
Ile Ser Gly Gln Cys His Cys Val Asp Ser Tyr Thr Gly Pro Thr Cys
        260             265             270
Arg Glu Val Pro Thr Gln Leu Ser Ser Ile Arg Pro Ala Pro Gln His
    275             280             285
Ser Ser Ser Lys Ala Met Lys His
    290             295
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1011c2PCTSEQUENCE LISTING

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        <211> 106
        <212> PRT
        <213> Mouse


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1               5                   10                  15
Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu
            20                  25                  30
Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Tyr
        35                  40                  45
Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Ser
    50                  55                  60
Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Ile Cys Ile Asn
65                  70                  75                  80
Pro Asp Pro Glu Lys Arg Pro Asp Ile Ala Tyr Val Tyr Asp Val Ala
                85                  90                  95
Lys Arg Met His Ala Cys Thr Ala Ser Thr
            100                 105

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        <211> 53
        <212> PRT
        <213> Mouse


        <400> 460
Met Cys Ala Gly His Gly Gln Ser Leu Leu Ile Ala Ser Asp Asp Gly
1               5                   10                  15
Arg Val Ser Arg Gln Pro Trp Ser Cys Leu Asn Ile Val Ser Asn Cys
            20                  25                  30
His Ser Phe Arg Glu Arg Gly Thr Ser Ser Pro Leu Leu Leu Ala Leu
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    50

        <210> 461
        <211> 261
        <212> PRT
        <213> Mouse


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1               5                   10                  15
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            20                  25                  30
Gly Pro Arg Ile Gly Arg Pro Trp Gly Trp Glu Gly Pro His His His
        35                  40                  45
His His Leu Ala Ser Gly Ser His Lys Pro Leu Pro Leu Leu Thr His
    50                  55                  60
Arg Phe Pro Phe Tyr Tyr Glu Phe Lys Met Ala Phe Val Leu Trp Leu
65                  70                  75                  80
Leu Ser Pro Tyr Thr Lys Gly Ala Ser Leu Leu Tyr Arg Lys Phe Val
                85                  90                  95

1011c2PCTSEQUENCE LISTING

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His Pro Ser Leu Ser Arg His Glu Lys Glu Ile Asp Ala Cys Ile Val
            100             105                 110
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            115             120                 125
Ser Leu Asn Ile Ala Ala Ser Ala Ala Val Gln Ala Ala Thr Lys Ser
            130             135                 140
Gln Gly Ala Leu Ala Gly Arg Leu Arg Ser Phe Ser Met Gln Asp Leu
145             150             155                 160
Arg Ser Ile Pro Asp Thr Pro Val Pro Thr Tyr Gln Asp Pro Leu Tyr
                165             170                 175
Leu Glu Asp Gln Val Pro Arg Arg Arg Pro Pro Ile Gly Tyr Arg Pro
            180             185                 190
Gly Gly Leu Gln Gly Ser Asp Thr Glu Asp Glu Cys Trp Ser Asp Asn
            195             200                 205
Glu Ile Val Pro Gln Pro Pro Val Gly Pro Arg Glu Lys Pro Leu Gly
210             215                 220
Arg Ser Gln Ser Leu Arg Val Val Lys Arg Lys Pro Leu Thr Arg Glu
225             230                 235                 240
Gly Thr Ser Arg Ser Leu Lys Val Arg Thr Pro Lys Lys Ala Met Pro
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            20                  25                  30
Lys Ser Lys Cys Thr Gly Gly Leu Gln Pro Pro Val Gln Tyr Glu Asp
            35              40                  45
Val His Thr Asn Pro Asp Gln Asp Cys Cys Leu Leu Gln Val Thr Thr
        50              55                  60
Leu Asn Phe Ile Phe Ile Pro Ile Val Met Gly Met Ile Phe Thr Leu
65                  70                  75                  80
Phe Thr Ile Asn Val Ser Thr Asp Met Arg His His Arg Val Arg Leu
                85                  90                  95
Val Phe Gln Asp Ser Pro Val His Gly Gly Arg Lys Leu Arg Ser Glu
            100                 105                 110
Gln Gly Val Gln Val Ile Leu Asp Gln Cys Thr Ala Phe Gly Ser Leu
            115                 120                 125
Thr Gly Gly Ile Leu Ser Thr His Ser Pro
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        <210> 463
        <211> 314
        <212> PRT
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1011c2PCTSEQUENCE LISTING

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                20                      25                      30
Lys Asn Leu Leu Pro Glu Thr Thr Tyr Arg Ile Arg Ile Gln Ala Ile
            35.                     40                      45
Asn Glu Ile Gly Val Gly Pro Phe Ser Gln Phe Ile Lys Ala Lys Thr
        50                      55                      60
Arg Pro Leu Pro Pro Ser Pro Pro Arg Leu Glu Cys Ala Ala Ser Gly
65                      70                      75                      80
Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser Asn Ser Lys Thr His
                85                      90                      95
Ala Ala Gly Asp Met Val Tyr Thr Leu Gln Leu Glu Asp Arg Asn Lys
            100                     105                     110
Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His Thr Tyr Lys Val Gln
            115                     120                     125
Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg Ile Gln Ala Met Ser
            130                     135                     140
Glu Ala Gly Glu Gly Pro Tyr Ser Glu Thr Tyr Thr Phe Ser Thr Thr
145                     150                     155                     160
Lys Ser Val Pro Pro Thr Leu Lys Ala Pro Arg Val Thr Gln Leu Glu
                165                     170                     175
Gly Asn Ser Cys Glu Ile Phe Trp Glu Thr Val Pro Pro Met Arg Gly
            180                     185                     190
Asp Pro Val Ser Tyr Val Leu Gln Val Leu Val Gly Arg Asp Ser Glu
            195                     200                     205
Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr Phe Gln Ile Ser Gly
    210                     215                     220
Leu Gln Ser Asn Thr Asp Tyr Arg Phe Arg Val Cys Ala Cys Arg Arg
225                     230                     235                     240
Cys Val Asp Thr Ser Gln Glu Leu Ser Gly Ala Phe Ser Pro Ser Ala
                245                     250                     255
Ala Phe Met Leu Gln Gln Arg Glu Val Met Leu Thr Gly Asp Leu Gly
            260                     265                     270
Gly Met Glu Glu Ala Lys Met Lys Gly Met Met Pro Thr Asp Glu Gln
        275                     280                     285
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        180
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1011c2PCTSEQUENCE LISTING
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600
aagacaaatt atatattgct atgaagctct tcttaccagg gtcagttttt acattttata
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1320
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1380
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gacgatcctg cgccctgccc tctcctgtgt acatattgcc ttcagtaccc ctcccccacc
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1560
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1663

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<211> 99
<212> PRT
<213> Mouse

<400> 465
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1011c2PCTSEQUENCE LISTING

| 1 | | | | | 5 | | | | | 10 | | | | | 15 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Ala | Ser | Arg | Val | Asp | Gly | Ser | Lys | Cys | Lys | Cys | Ser | Arg | Lys | Gly | Pro |

|  | | 20 | | | | | 25 | | | | | 30 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Lys | Ile | Arg | Tyr | Ser | Asp | Val | Lys | Lys | Leu | Glu | Met | Lys | Pro | Lys | Tyr |

|  | | 35 | | | | | 40 | | | | | 45 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Pro | His | Cys | Glu | Glu | Lys | Met | Val | Ile | Val | Thr | Thr | Lys | Ser | Met | Ser |

|  | | | | 50 | | | | | 55 | | | | | 60 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Arg | Tyr | Arg | Gly | Gln | Glu | His | Cys | Leu | His | Pro | Lys | Leu | Gln | Ser | Thr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

|  | | | | 85 | | | | | 90 | | | | | 95 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Lys | Arg | Phe | Ile | Lys | Trp | Tyr | Asn | Ala | Trp | Asn | Glu | Lys | Arg | Arg | Val |

| Tyr | Glu | Glu |
|---|---|---|

1

(51) International Patent Classification⁷: C07K 14/47, 14/485, 14/515, 7/06, C12N 15/63, 15/85, A61K 38/08, 38/17, A61P 17/00, 25/00, 29/00, 35/00, 43/00

(21) International Application Number: PCT/NZ00/00075

(22) International Filing Date: 15 May 2000 (15.05.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/312,283          14 May 1999 (14.05.1999)     US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(54) Title: COMPOSITIONS ISOLATED FROM SKIN CELLS AND METHODS FOR THEIR USE

(57) Abstract: Isolated polynucleotides encoding polypeptides expressed in mammalian skin cells are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

| A. | CLASSIFICATION OF SUBJECT MATTER |
|---|---|

Int. Cl. [7]:     C07K 14/47, 14/485, 14/515, 7/06; C12N 15/63, 15/85, A61K 38/08, 38/17; A61P 17/00, 25/00, 29/00, 35/00, 43/00.

According to International Patent Classification (IPC) or to both national classification and IPC

| B. | FIELDS SEARCHED |
|---|---|

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
ANGIS: Sequence search; ID No. 187, 196, 342, 343, 395, 397, 398.

| C. | DOCUMENTS CONSIDERED TO BE RELEVANT |
|---|---|

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X | Biochemical and Biophysical Chemical Research Communications. 225:703-706 (1999)<br>Hromas, R et al<br>"Cloning of BRAK, a Novel Divergent CXC Chemokine Preferentially Expressed in Normal versus Malignant Cells"<br>See Figure 1, Table 1. Sequence ID No. 397 and No. 398, both 100%. | 1-8, 13-14, 15-16, 17, 23, 25 |
| P,X | *J Immunol* 2000 Sep 1;165(5):2588-95<br>Cao X, Zhang W, Wan T, He L, Chen T, Yuan Z, Ma S, Yu Y, Chen G<br>"Molecular cloning and characterization of a novel CXC chemokine macrophage inflammatory protein-2 gamma chemoattractant for human neutrophils and dendritic cells."<br>See whole document.<br>Sequence ID No. 397 and No. 398, both 100% homology. | 1-28 |

☐ Further documents are listed in the continuation of Box C     ☐ See patent family annex

| * | Special categories of cited documents: | "T" | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
|---|---|---|---|
| "A" | document defining the general state of the art which is not considered to be of particular relevance | | |
| "E" | earlier application or patent but published on or after the international filing date | "X" | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| "L" | document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | "Y" | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| "O" | document referring to an oral disclosure, use, exhibition or other means | | |
| "P" | document published prior to the international filing date but later than the priority date claimed | "&" | document member of the same patent family |

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 12 October 2000 | 7 NOV 2000 |
| Name and mailing address of the ISA/AU | Authorized officer |
| AUSTRALIAN PATENT OFFICE<br>PO BOX 200, WODEN ACT 2606, AUSTRALIA<br>E-mail address: pct@ipaustralia.gov.au<br>Facsimile No. (02) 6285 3929 | *[signature]*<br>**IAN DOWD**<br>Telephone No : (02) 6283 2273 |

| Box I | Observations where certain claims were found unsearchable (Continuati n of item 2 of first sheet) |
|---|---|

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :

   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos :

   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos :

   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

| Box II | Observations where unity of invention is lacking (Continuation of item 3 of first sheet) |
|---|---|

This International Searching Authority found multiple inventions in this international application, as follows:

   See supplemental sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to:

   The invention as it is exemplified by amino acid sequence ID No.s 187, 196, 342, 343, 395, 397, and 398.

**Remark on Protest**     ☐ The additional search fees were accompanied by the applicant's protest.

                          ☐ No protest accompanied the payment of additional search fees.

**Supplemental Box**
(To be used when the space in any of Boxes I to VIII is not sufficient)

**Continuation of Box No: II**

This international application does not comply with the requirement of unity of invention because it does not relate to one invention or to a group of invention so linked as to form a single general inventive concept:

(1) The international application has claimed nucleic acid sequences encoding 4 enzymes and 31 proteins, the fragments, complements, reverse complements and reverse sequences of these genes, expression vectors of the sequences, transformed host cells, methods for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularization of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of HIV-1 to leukocytes, treatment of inflammatory and neurological diseases and cancer, and polypeptides coded by these genes and their variants with at least 50%, 75% or 90% identity.

(2) Whilst the 465 sequences are from skin cells, the claims are defined as to these sequences per se and their variants which have 50%, 75% or 90% identity. The invention as claimed is also to the various methods of use (as indicated above) based on these sequences. It is clear that all these nucleic acid sequences are not limited to the source from which they are isolated, as such the source from skin cells can not be the special technical feature under Rule 13.2 of the PCT.

(3) The nucleic acid sequences and their putative amino acid sequences have been shown to have similarity to proteins or enzymes which are known (see Table 2 pages 24 to 25 of the description). Based on this methodology, the 465 sequences have been assigned to 31 proteins and 4 enzymes. However, these proteins and enzymes are not unified by sequence homology, by a common substrate or their mode of action. Additionally, many of these proteins or enzymes are known to have activity not directly associated with epithelial cells. Therefore, the use of nucleotide sequences encoding these proteins and enzymes , either in the sense or anti-sense direction, is not a special technical feature under Rule 13.2 of the PCT.

For the above reasons, this international application does not comply with the requirements of unity of invention.

The International Searching authority has found that there are 34 separate inventions, wherein a single protein or enzyme provides the special technical feature.

1.    Polynucleotide Sequence ID No. 118 and amino acid Sequence ID No. 196 and their at least 50% identity homologues, encoding human TR1.

2.    Polynucleotide Sequence ID No. 68, 437 and amino acid Sequence ID No. 187 and their at least 50% identity homologues, encoding transforming growth factor alpha, murine TR1.

3.    Polynucleotide Sequence ID No. 119 and amino acid Sequence ID No. 197 and their at least 50% identity homologues, encoding DP3.

4.    Polynucleotide Sequence ID No. 271 and amino acid Sequence ID No. 345 and their at least 50% identity homologues, encoding MURINE KS1.

5.    Polynucleotide Sequence ID No. 272 and amino acid Sequence ID No. 346 and their at least 50% identity homologues, encoding human KS1.

**Supplemental Box**
(To be used when the space in any of Boxes I to VIII is not sufficient)

## Continuation of Box No: II

6.    Polynucleotide Sequence ID No. 273 and amino acid Sequence ID No. 347 and their at least 50% identity homologues, encoding KS2.

7.    Amino acid Sequence ID No. 129 and their at least 50% identity homologues, encoding KS3.

8.    Polynucleotide Sequence ID No. 64 and 372 and amino acid Sequence ID No. 183 and 396 and their at least 50% identity homologues, encoding Slit (a secreted molecule required for CNS development).

9.    Polynucleotide Sequence ID No. 65 and amino acid Sequence ID No. 184 and their at least 50% identity homologues, encoding an immunogobulin receptor.

10.    Polynucleotide Sequence ID No. 66, 403 and amino acid Sequence ID No. 185, 409 and their at least 50% identity homologues, encoding RIP protein kinase.

11.    Polynucleotide Sequence ID No. 67 and amino acid Sequence ID No. 186 and their at least 50% identity homologues, encoding extracellular protein.

12.    Polynucleotide Sequence ID No. 69 and amino acid Sequence ID No. 188 and their at least 50% identity homologues, encoding DRS protein.

13.    Polynucleotide Sequence ID No. 70 and amino acid Sequence ID No. 189 and their at least 50% identity homologues, encoding A33 receptor.

14.    Polynucleotide Sequence ID No. 71 and amino acid Sequence ID No. 190 and their at least 50% identity homologues, encoding IL-12 alpha sub-unit.9. Polynucleotide Sequence ID No. 72 and amino acid Sequence ID No. 191 and their at least 50% identity homologues, encoding TNF receptor.

15.    Polynucleotide Sequence ID No. 73, 438 and amino acid Sequence ID No. 192, 458 and their at least 50% identity homologues, encoding epidermal growth factor.

16.    Polynucleotide Sequence ID No. 74 and amino acid Sequence ID No. 193 and their at least 50% identity homologues, encoding fibronectin type III receptor.

17.    Polynucleotide Sequence ID No. 75, 439 and amino acid Sequence ID No. 194, 459 and their at least 50% identity homologues, encoding serine/threonine kinase.

18.    Polynucleotide Sequence ID No. 76 and amino acid Sequence ID No. 195 and their at least 50% identity homologues, encoding immunoglobulin receptor.

19.    Polynucleotide Sequence ID No. 254 and amino acid Sequence ID No. 331 and their at least 50% identity homologues, encoding immunoglobulin-like receptor.

20.    Polynucleotide Sequence ID No. 255 and amino acid Sequence ID No. 332 and their at least 50% identity homologues, encoding epidermal growth factor.

21.    Polynucleotide Sequence ID No. 256 and amino acid Sequence ID No. 333 and their at least 50% identity homologues, encoding serine/threonine kinases.

**Supplemental Box**

(To be used when the space in any of Boxes I to VIII is not sufficient)

**Continuation of Box No:**

22. Polynucleotide Sequence ID No. 257 and amino acid Sequence ID No. 334 and their at least 50% identity homologues, encoding protein kinase.

23. Polynucleotide Sequence ID No. 258 and amino acid Sequence ID No. 335 and their at least 50% identity homologues, encoding notch family proteins.

24. Polynucleotide Sequence ID No. 259 and amino acid Sequence ID No. 336 and their at least 50% identity homologues, encoding extracellular protein with epidermal growth factor domain.

25. Polynucleotide Sequence ID No. 260, 453 and amino acid Sequence ID No. 337, 463 and their at least 50% identity homologues, encoding fibronectin Type III receptor.

26. Polynucleotide Sequence ID No. 261 and amino acid Sequence ID No. 338 and their at least 50% identity homologues, encoding immunoglobulin receptor.

27. Polynucleotide Sequence ID No. 262, 454 and amino acid Sequence ID No. 339 and their at least 50% identity homologues, encoding ADP/ATP transporter.

28. Polynucleotide Sequence ID No. 263 and amino acid Sequence ID No. 340 and their at least 50% identity homologues, encoding mouse CXC chemokine.

29. Polynucleotide Sequence ID No. 264 and amino acid Sequence ID No. 341 and their at least 50% identity homologues, encoding nucleotide sugar transporter.

30. Polynucleotide Sequence ID No. 365 and amino acid Sequence ID No. 389 and their at least 50% identity homologues, encoding TGF-betas.

31. Polynucleotide Sequence ID No. 366 and amino acid Sequence ID No. 390 and their at least 50% identity homologues, encoding integrins (membrane protein).

32. Polynucleotide Sequence ID No. 367 and amino acid Sequence ID No. 391 and their at least 50% identity homologues, encoding integrins.

33. Polynucleotide Sequence ID No. 368 and amino acid Sequence ID No. 392 and their at least 50% identity homologues, encoding cell wall protein precursor.

34. Polynucleotide Sequence ID No. 369 and amino acid Sequence ID No. 393 and their at least 50% identity homologues, encoding HT protein.